us-10-600-230-1.rge

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Title:
Perfect score:
Sequence: OM nucleic - nucleic search, using sw model Run on: Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Scoring table: Database : Minimum DB seq length: 0
Maximum DB seq length: 200000000 Total number of hits satisfying chosen parameters: Searched: GenEmbl:*
1: gb_ba:*
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3: gb_env:* IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-10-600-230-1 485 December 28, 2005, 08:02:56; Search time 2756 Seconds (without alignments) 10003.292 Million cell updates/sec 5883141 seqs, 28421725653 residues 1 gcgcgcggaaggaaagt.....cctccaaatgatgaggtacc 485 GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. gb_om: *
gb_pat: * 11766282

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	9.9	10.0	10.1	10.3	10.4	10.6	10.6	10.6	10.6	10.6	10.8	13.0	39.3	58.6	59.3	92.0	97.9	97.9	Query Match	æ
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BX537162	CR749178	AX458482	CR383681	CR407564	BX293540	AC023534	AL928920	AC158414	AC155816	AC122434	BX247871	PFA929355	AE014827	AE014835	AX251775	AX345620	CR456634	AC099738	CR847971	AC132600	BX842571	AC005036	AY701231	CR376799	CNS06K1D	CR354537
BX537162 Zebrafish	CR749178 Danio rer	AX458482 Sequence	CR383681 Danio rer	CR407564 Danio rer	BX293540 Zebrafish	AC023534 Homo sapi	AL928920 Zebrafish	AC158414 Pongo	AC155816 Mus muscu	AC122434 Mus muscu	BX247871 Zebrafish	AL929355 Plasmodiu		AE014835 Plasmodiu	AX251775 Sequence	AX345620 Sequence	CR456634 Macropus	AC099738 Homo sapi	CR847971 Danio rer	AC132600 Mus muscu	BX842571 Zebrafish		AY701231 Orconecte	CR376799 Danio rer	AL402311 T3 end of	CR354537 Danio rer

ALIGNMENTS

CDS	gene	promoter	FEATURES source		TITLE	REFERENCE	JOURNAL PUBMED	TITLE	REFERENCE	SOURCE ORGANISM	VERSION VERSION KEYWORDS	RESULT 1 SCAL1 LOCUS DEFINITION
/gene="CAL1" 2793578 /gene="CAL1" /gene="CAL1" /BC number="2.4.1.16" /codon_start=1 /evidence=experimental		er 240244 /note="TATA-like box" er 253257	Location/Qualifiers 14046	Biologia,	Direct Submission Submitted (16-JAN-1991) A. Duran. Instituto de Microbiologia	2 (bases 1 to 4046) Duran.A.	Saccharomyces cerevisiae J. Cell Biol. 114 (1), 101-109 (1991) 2050737	CAL1, a gene required for activity of chitin synthase 3 in	omycotina; ; Saccharc	Saccharomyces cerevisiae (baker's yeast) Saccharomyces cerevisiae	X57300.1 GI:3359 CAL1 gene; chitin synthase 3.	SCAL1 SCAL1 4046 bp DNA linear PLN 02-AUG-1991 Saccharomyces cerevisiae CAL1 gene for chitin synthase 3.

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DEFINITION
ACCESSION
VERSION
                                                                                                                                                                            RESULT 2
SCGAL1/c
LOCUS
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                                                                                                                   33117 bp
S.cerevisiae (alphaS288C) GAL1,
X76078
X76078.1 GI:498748
CAL1 gene; chitin synthase 3; FUR4 gene; GAL1 gene; galactokinase; ribosomal protein L2B; uracil permease; YBR0304 gene; YBR0308 gene; YBR0310 gene; YBR0312 gene; YBR0313 gene; YBR0314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAA 3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGG 185
                                                                                                                                                                                                                                                                                                                                                            TGTATAATTCAAAATACTTTGCTTTTCTCCATGACTTGAACCTCCAAATGATGAGGTA 483
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CHTSKEDRDAFYGLKSKADVYFFWDGIKNSSRNLIVXNGDGSKFUNGCIASDVLYVS
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GMTTMTTQNAWKLSNENKAVHSRNPSTLLPTSSMFWNKATSSPVPGSSLIQSLDSTII
HPDIVQQPPLDFWFYGFPLIHTICFVTCYSEDEEGLRTIDSIGSTDYPNSKKLLMVV
VGCTIVCTORDIALTMACKAVHSRNPSTLLPTSSMFWNKATSSPVRGSKKLLMVV
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ICFTIYVIIFALVSKYPPVITLVLLAIILGLPGLIVJTATRWSYLWMMCVYICALPI
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NRKEESDSFVA"
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Pred. No. 3.4e-80;
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Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Saccharomyceta; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (11-NOV-1993) P.H.M. Smits, University of Amsterdam,
Section for Molecular Biology, Department of Molecular Cell
Biology, Kruislaan 318, 1098 SM Amsterdam, NETHERLANDS
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 33117)
Smits,P.H.M., de Hann,M., Maat,C. and Grivell,L.A.
The complete sequence of a 33 kb fragment on the right arm of chromosome II from Saccharomyces cerevisiae reveals 16 open reading frames, five previously identified genes and a homologue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smits, P.H.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Saccharomyces cerevisiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="FUR4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="GAL1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _xref="taxon:4932"
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CDS

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                                                                                                                                                                                                         ELDRLTYWISELDDKDHIKIQPLFISCDPARDTPDVLKEYLSDFHPAIIGLTGTYDQV
KSVCKKYKVYFSTPRDVKPNQDYLVDHSIFFYLIDPEGQFIDALGRNYDEQSGLEKIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFEREDILNRKEESDSFVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA53680.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="CAL1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (7577. .11074)
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                                                                                                                             complement (13830. .15014)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="CAL1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _xref="GOA:P38218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _xref="InterPro:IPR001199"
xref="InterPro:IPR006073"
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Matches
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                                                                                                                                                                                                                                                                  7549
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                                                                                                                                                   186
306 TTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTTC 365
                                                                                                                                                                                                                                                                                                                                                                                                                        476;
                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                         GCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAA
                                                                                                                                       CTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACAC
                                                                                                                                                                                         CTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGG
                                                                                                                                                                                                              CTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGG
                                                                                                                                                                                                                                                                  CGGAAGGAGAAAGTGACTCCTTCGTTGCATAGACAGTATGAAAATATTTTTACTGTGAT
                                                                                                                                                                                                                                                                                                                                                                CGGAAGGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAAATATTTTTACTGTGAT
                                                                                                               CTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACAC
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gene

Sg

Conservative

0

2

Indels

0

Gaps

7490

125

245 7430 185 7550

65 0

7310 305 7370 Length 33117;

97.9%;

Score 474.8; DB 15; Pred. No. 1.8e-80; Mismatches

٧

CDS gene

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QKALEGABKIAKRGGQSLEVKQKKEMDLITKIIKLLESGQRVANHSWTSKEVEIINS
MFLLTAKPCIVINLASERDYIRKKNHHLLRIKEWDDKYSPGDLIIPFSVSLEERLSHM
SPEDABEEELKKLQTISALPKIITTMRQKLDLISFFTCGPDEVREWTIRRGTKAFQAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GHIISPRDEIETLTWNTNTTTDEQLLELVKKGITGKGKKKKVVVLEW"
complement (17574. .19151)
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complement (17574. .19151)
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/db_xref="UniProt/Swiss-Prot:P38070"
/db_xref="UniProt/Swiss-Prot:P38070"
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RLSITPQDIISSNIGENELSRNLHDFKPVRVLGQGAYGKVLLVKDVNTSKLYAMKQLR
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YSFHDNSKLYLLLQYIPGGELFYHLKEHGTLDETTVSFYAABISCALRFLHTKGVVYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (16026. .17168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIHNDLMNTFILAQVMKCEDVFEYKDDSAIKAAGKLMQKGKDYVVEDGDIIYFRAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="YBR0310"
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CDS	REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	TITLE	RESULT 3 SCYBR022W/c LOCUS DEFINITION ACCESSION VERSION VERSION VERSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS	Db 73 Qy 3 Db 72 Qy 4 Db 71
Pr ro	Crivel, L.A., de Hann, M., M. Unpublished (bases 1 to 1089) MIPS. Direct Submission Submitted (30-AUG-1994) Data European yeast chromosome I. MAx-Planck-Institut fuer Binder Submission Location/Qualifier 1. 1089 /organism="Sacchar	Brendel, M., Brueckner, M., Bussereau, F., Christiansen, C., Contreras, R., Crouzet, M., Cziepluch, C., Demolis, N., Delaveau, T., Doignon, F., Domdey, H., Duesterhus, S., Dubois, E., Dujon, B., El Bakkoury, M., Entian, K.D., Feuermann, M., Fiers, W., Fobo, G.M., Fritz, C., Gassenhuber, H., Glansdorff, N., Goffeau, A., Grivell, L.A., de Haan, M., Hein, C., Herbert, C.J., Hollenberg, C.P., Hollmstrom, K., Jacq, C., Jacquet, M., Jauniaux, J.C., Jonniaux, J.L., Kallesoe, T., Kiesau, P., Kirchrath, L., Koetter, P., Korol, S., Liebl, S., Logghe, M., Lohan, A.J.B., Louis, E.J., Li, Z.Y., Maatr, M.J., Mallet, L., Mannhaupt, G., Messenguy, F., Miosga, T., Molemans, F., Mueller, S., Mass, F., Obermaler, B., Perea, J., Pierard, A., Piravandi, E., Pohl, F.M., Pohl, T.M., Potier, S., Proft, M., Purnelle, B., Ramezani Rad, M., Rieger, M., Rose, M., Schaaff-Gerstenschlaeger, I., Scherens, B., Schwarzlose, C., Skala, J., Slonimski, P.P., Smits, P.H. M., Souciet, J.L., Steensma, H. Y., Stucka, R., Urrestarazu, A., van der Aatt, Q.J., van Dyck, L., Vassarotti, A., Vetter, I., Vierendeels, F., Vissers, S., Wagner, G., de Wergifosse, P., Wolfe, K.H., Zagulski, M., Zimmermann, F.K., Mewes, H.W. and Kleine, K. Complete DNA sequence of yeast chromosome II	SCYBR022W S.cerevisiae chromosome II reading frame ORF YBR022w. S.5591 Y13134 Z35891 Y13134 Z35891.1 GI:536227 Saccharomyces cerevisiae (baker's yeast) Saccharomyces cerevisiae Eukaryota; Fungi; Ascomycota; Saccharomyces carevisiae Eukaryota; Fungi; Ascomycota; Saccharomyces. Saccharomycetales; Saccharomycetaceae; Saccharomyces. 1 Feldmann, H., Aigle, M., Aljinovic, G., Andre, B., Baclet, M.C., Beatharomyces.	7309 Triátafricectiarrisistriciarisistes (250) 366 ACTTGTTCGAGTTTTGTCTTTGCTTCTAAAGGTCTTCAATTTATCTAAAGCAAGTTT 425

670

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Best Local Similarity
Matches 447; Conserv
                                                                                                                                                                                                                                                                                                                                                1029
                                                                                                                                                                                                                                                                                                                                                                                                       1089 TAGACAGTATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             447; Conservative
                                                                                                                                                                      849
                                                                                                                                                                                                                               909
669
                           456
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                                                                                                                                          336
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                                                                                                                                                                                                                                                                                       969
                                                                                                                                                                                                                                                                                                                  156
                                                                                                                                                                                                                                                                                                                                                               36 TAGACAGTATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGAA 95
                                                                                                                                                                                     TATGCCACTATTTATCTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTG 335
                                                                                                                                                                                                                                                                                                                                              PARGGTCTTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTTGCTTTTCTCC
                                                                                                                            GCCGTTTAAATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCT
                                                                                                                                                                                                                                              ACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAA 275
                                                                                                                                                                                                                                                                                        TCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAA
                                                                                                                                                                                                                                                                                                         TCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAA 215
ATGACTTGAACCTCCAAATGATGATGTA 642
                ATGACTTGAACCTCCAAATGATGAGGTA 483
                                                                                    AAAGGTCTTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTTTCTCC 455
                                                                                                                GCCGTTTAAATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTTGCTTCTCT
                                                                                                                                                                        TATGCCACTATTTATCTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTG
                                                                                                                                                                                                                               ACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVLEEFSGDMSFTVYQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 446.4; DB 1
Pred. No. 1.1e-74;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15; Length 1089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                               850
                                                                                                                                                                                                                                                                                        910
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1030

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970

RESULT 4 AY557705/c LOCUS ACCESSION VERSION KEYWORDS SOURCE ORGANISM JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS DEFINITION COMMENT TITLE JOURNAL TITLE Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 534)
Marsischky,G., Rolfs,A., Richardson,A., Kane,M., Baqui,M.,
Taycher,E., Hu,Y., Vannberg,F., Weger,J., Kramer,J., Moreira,D.,
Taycher,E., Zuo,D., Raphael,J., Hogle,C., Jepson,D., Williamson,J.,
Kelley,F., Zuo,D., Raphael,J., Hogle,C., Jepson,A., Kolodner,R.,
Camargo,A., Gonzaga,L., Vasconcelos,A.T., Simpson,A., Kolodner,R.,
Harlow,E. and LaBaer,J.
Harlow,E. and LaBaer,J.
Creation of the YFLEX clone resource: cloning of Saccharomyces
cerevisiae ORFs in the Gateway recombinational cloning system 2 (bases 1 to 534)
Marsischky,G., Rolfs,A., Richardson,A., Kane,M., Baqui,M.,
Marsischky,G., Rolfs,A., Richardson,A., Kramer,J., Moreira,D.,
Taycher,E., Hu,Y., Vannberg,F., Weger,J., Kramer,J., Moreira,D.,
Kelley,F., Zuo,D., Raphael,J., Hogle,C., Jepson,D., Williamson,J.,
Camargo,A., Gonzaga,L., Vasconcelos,A.T., Simpson,A., Kolodner,R.,
Harlow,E. and LaBaer,J. AY557705.1 GI:452 Yeast ORF Project. AY557705 534 bp DNA linear PLN 14-MAR-2004 Saccharomyces cerevisiae clone FLH000707.01X YBR022W gene, complete Submitted (17-FEB-2004) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA This clone is part of a collection of Saccharomyces cerevisiae full-length ORF clones generated by the Harvard Institute of Unpublished
2 (hases 1 GI:45269300

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
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                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                    ACCESSION
JOURNAL
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195
                  CSD2, CSD3, and CSD4, genes required for chitin synthesis i Saccharomyces cerevisiae: the CSD2 gene product is related chitin synthases and to developmentally regulated proteins Rhizobium species and Xenopus laevis
MOL. Cell. Biol. 12 (4), 1764-1776 (1992)
                                                                                                                                                                                                                                                                                                                 S.cerevisiae CSD2 gene complete cds.
M73697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the ORFs, including a Kozak consensus sequence);
'ATCCCCGGGAATTGCCATG' after the stop codon and before the attL2
site (from the Research Genetics primers used to amplify the ORFs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteomics. Each CDS has been cloned with its native stop-codon. The CDS has been directionally cloned using the Gateway cloning system into the donor vectors pDONR 201 or pDONR 221. Additional sequences in the clone: 'TCCAGCTGACCACC' after the attll site and before the 'ATG' (from Research Genetics primers used to amplify
                                                                                                                                                                                                                                                                     M73697.1 GI:172103 chitin synthase.
                                                                                                              Bulawa, C.E.
CSD2, CSD3,
                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 4345)
                                                                                                                                                                                                                        Saccharomyces cerevisiae (baker's yeast)
Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                   YSCPCHSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAATACTTTGCTTTTCTCCATGACCTTGAACCTCCAAATGATGATGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAS56031.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="YBR022W"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="Escherichia coli DH5alpha T1 resistant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Saccharomyces cerevisiae"
/mal_type="genomic DNA"
/mal_type="fenomic DNA"
/db xref="teaxon:4932"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                            putative chitin synthase)
                                                                                                                                                                                                                                                                                                                                                                                   DNA
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                                                               synthesis in is related to proteins in
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    Matches
                                                    Query Match
Best Local :
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                                                    Local Similarity
286;
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              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           /translation="myglugddpddyyluluqdbesillrsrhsygsgaphrqgslyrb |
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/translation="myglugddpddyyluluqbesillrsrhsyslskgsygskesg |
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ETNDTLSFWQMYCYFITFWAPAPILAFCGMPKKERQMAWREKVALISVILYIGAIVAF |
LTFGFTKTVCSSSKLRLKNNEVSTEFVVINGKAYELDTSSRGGIQDVEVDSDTLYGFW |
LTFGFTKTVCSSSKLRLKNNEVSTEFVVINGKAYELDTSSRSGGIQDVEVDSDTLYGFW |
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VENYAGWNCHTSKEDRDAFYGLKSKADVYFTWDGIKNSSRNLITVNGDVLDLDLLDWL |
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QSLDSTIIHPDIVQQPPLDFMPYGFPLIHTICFTVTSSEDEBGLRTTLDSLSTTDYPN |
SHKLLMVVCDGLIKGSGNDKTTPBIALGMNDDFVTPPDEVKPYSYVAVASGSKRHMMA |
KITAGEFYKNDDSTIPPENQQRVPIITIVKCGTPAEGCAAKFGNRGKRBSQIILMSETLB |
KITPDERMTQLEFQLLKNINGITGLMADFYETVLMVDADTKVPPDALTHNVAEMVKDF |
KITPDERMTQLEFQLLKNINGITGLMADFYETVLMVDADTKVPPDALTHNVAEMVKDF |
KRSSDGYWPVLANDFYLSTYIISHQAKAFESVFGSVTCLPGCFSMYRIKS |
PKRSSDGYWPVLANDFYSYSDANDHYNTLHKKNLLLLGERGKBSTTGYFRKQVF |
FRESSDGYWPVLANDFYSYSDANDHYNTLHKKNLLLLGERGKBSTTGYFRKQVF |
FRESSDGYWPVLANDFYSTANDHYNTLHKKNLLLLLGERGKBSTTGYFRKQVF |
FRESSDGYWPVLANDFYSTANDHYNTLHKKNLLLLLGERGKRBSTGTFKFKRQVF |
FRESSDGYWPVLANDFYTTHFFT |
FRESSDGYMPVLANDFYTTHFFT |

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/function="Required for chitin synthesis in vivo and for chitin synthase Illactivity in vitro."
/note="'Deduced amino acid sequence of CSD2 has limited, butstatisticallysignificant similarity to chitin synthases, to the nodC protein of Rhizobiumand to the DG42 protein of X. laevis'; putative"
                                                                                                                                                                                                                                                                                                                               VPKAACKTIAPDKFKVLLSQRRRWINSTVHNLFELVLIRDLCGTFCFSMQFVIGIELI
GTMVLPLAICFTIYVIIFAIVSKPTPVITLVLLAIILGLPGLIVVITATRWSYLWWMC
                                                                                                                                                                                                                                              EFEREDILNRKEESDSLVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="chitin synthase"
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/db_xref="GI:172104"
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old_type="genomic DNA"

old_xref="taxon:4932"
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    Score 284.2; DB 1
Pred. No. 3.4e-44;
0; Mismatches 3
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SCYBR023C
S.cerevisiae chromosome
Z35892 Y13134
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                                                                                                                                                                                                                                                                                                                       CGGAAGGAGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTTACTGTGAT
                                                                                                           GCGTTCTGTCTTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGT
                                                                                                                                                                                              CTTAGAACTTAATAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGG
                                                                                                                                                                                                                                                                             GCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGT
                                                                                                                                             TTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACAC
                                                                                                                                                                   CTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACAC
                                                                                                                                                                                                                        CTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGG
                                                                                                                                                                                                                                                  CGGAAGGAAGTGACTCCTTAGTTGCATAGACAGTATGAAAATATTTTTACTGTGAT
            5176 bp
II reading
               DNA linear I frame ORF YBR023c.
                           PLN 11-AUG-1997
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GI:536229

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AUTHORS
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TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (30-AUG-1994) Data collected by MIPS on behalf of the Submitted (30-AUG-1994) Data collected by MIPS on behalf of the European yeast chromosome II sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152 Martinsried, FRG; B-mail: Mewes@mips.embnet.org
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 5176)
Grivell,L.A., de Hann,M., Maat,M.J.
Unpublished
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VENYAGNNCHTSKEDRDAFYGLKSKADVYFTWDGI KNSSRNLI VNGDVLDLLDLLDL
EKDDVDYPVFDDLKTSNLQGYDLSLVLSNGHERKIARCLSBIIKVGENVSKTWGLID
EKDDVDYPVFDDLKTSNLQGYDLSLVLSNGHERKIARCLSBIIKVGENVSKTWDLSLDLA
SDVVLYVSLYFILSVVIIKFIIACYFRWTVARKGGAYIVDNKTMDKHTNDIEDWSNNI
QTKAPLKEVDPHLRPKKYSKKSLGHKAASTFDLLKKHSSKMFQFNESVILDTSMSSS
LQSSGSYRGMTTMTTQNAWKLSNENKAVHSRNESTLLFTSSMFWNKATSSPVPGSSLI
QSLDSTIIHPDLVQOFPLDFMYFGFPLHTICFVTCYSBDEBGLRTTLDSLSTTDYBN
SHKLLMVVCDGLIKGSGNDKTTPEIALGMMDDFVTPPDEVKPYSYVAVASGSKRHNMA
KIYAGFYKYDDSTIPPENQQRVPIITIVKCGTPAACQAAKFGNBGKRDSQIILMSFLE
KIYAGFYKYDDSTIPPENQQRVPIITIVKCGTPAACQAAKFGNBGKRDSQIILMSFLE
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DEFINITION ACCESSION VERSION

Plasmodium falciparum chromosome CR382399 AL844505 CR382399.1 GI:46361038

6

complete sequence; segment

INV 17-APR-2005 ce; segment 2/5.

DNA

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RESULT 7
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                                                                                                                                                                                                                                                                                                               CATTCAGAGTTCATACACAGTAAAATTCATAGATCTGTCATACTTCTTTAATACTTCCTC
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                                                                                                                                                                                                                                                      GGTTTCTGGCCAAGGGACTCCAAATATACCGCTATTGATTTTTGGCATCTCGAGCTTGTA 31387
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nilarity 53.4%;
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VPKAACKTIAPDKFKVLLSQRRRWINSTVHNLFELVLIRDLCGTFCFSMQFVIGIELI
GTMVLPLAICFTIYVIIFAIVSKPTPVITLVLLAIILGLPGLIVVITATRWSYLWWMC
VYICALPIWNFVLPSYAYWKFDDFSWGDTRTIAGGNKKAQDENEGEFDHSKIKWRTWR
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/note="ARS-consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-MAR-2004) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
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Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
Doggett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M.
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Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
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Eukaryota; Alveolata;
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Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                more information about this sequence or the Malaria Project, http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N., Pain, A., Berriman, M.,
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เล
                                                                                                                                                                                                                                                                                                         Complement (847. .1143)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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      .3403))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trust Genome Campus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harris, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anslini pkvllensgidi hqtifnvi dkynedrsepigi didtgepi i ahlkgi ydn
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                                                                                                                                                                                                                                                                                                                                                                 product="ornithine aminotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                          codon start=1
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                   BV061001 633 bp DNA linear (S212P6318FG5.TO CZECHII/Ei Mus musculus STS genomic,
tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                         TATTTATTATATGTATTTAAAAAAAAAAAAAAAAAAGTCTATATATTATTATATAT
                                                                                                                                                                                                                                                                                           ATTTATTTGAGAGGTATTTTAACACACCTTAGAACTTAAAACTTAAATAATAATATTTCT 158
                                                                                                                                                                                                                                                                                                                                                                                          ACAGTATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTT 98
                                                                                                                                                                                                                                                                                                                                                      ATATATATATATATATACAGCTAATATCAAGAAAATAAA 74939
                                                                                                                                                                                                         CTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACA 199
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KNOKKGKTSYLLDYYINEKTNMFGTYDYBKOLOKSINIA TOTOLOKOTOLOKUMISTOLOKUMINGING
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  gite.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIIMIYMBILKYINKNERIGVSLANKADEKYQKYEETNISTDKDDNASSDDNAGIIKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52.2; DB Pred. No. 0.63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 93"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
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                                                  STS 31-MAY-2003
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                          sequence
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VERSION
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AUTHORS
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ORIGIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C. Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers
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WGS-discovery: Paired-end low-coverage whole genome shotgun reads
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS
reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNI
detection was carried out by SSAHA-SNP. 225,000 reads were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer A: None
Primer B: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: kersli@genome.wi.mit.edu
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                                                                                                                                                                                                                              CAGTTATATTTTAATTCTTGTAATTTTTAGTATATGAAAATAATAAATTTTTAACTACTTTT
                                                                                                                                                                                                                                                                                   AACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATT
                                                                                                                                                                                                                                                                                                                                                                                                    GATATATGGTTGTGTGTAACTTATTTATTTGAGAGGTATTTTAACACACCCTTAGAACTAA 136
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                                                                                                             TAAATTAATATTTCTGAAAATTTTCTGGCATGTGTATTGTATTCACATCACTTTTACCCCT
                                                                                                                                                                      ACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCT
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CCTTCTCAATTTTACCCCTCCTTCAACCTCTTCCATTTGCCATTACCAGGTTCCATCACA 108
                                                     CTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAATTTATATTCCC 316
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/map="- 5 33-576 61053125-61052582"
/clone_lib="CZECHII/Ei"
<1. .>633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="CZECHII/Ei"
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REFERENCE AUTHORS TITLS JOURNAL REFERENCE AUTHORS TITLE	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS	RESULT 10 AC079954 LOCUS DEPINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
TX 77030, USA Human Genome Sequencing Center, Depar Genetics, Baylor College of Medicine, TX 77030, USA	dhyy, I., Charke, D., Chen, G., Chedhy, I., Christopoulos, C., Cleveland, thorne, S.R., David, R., David, M.L., Dich, D., Delaney, K.R., Delgado, O., mh, H.H., Douthwaite, K.J., Draper, H., K.J., Eagat, D., Edwards, Escotto, M., Falls, T., Ferraguto, D., ter, P., Frantz, P., Gabisi, A., Gao, J., ter, P., Frantz, P., Gabisi, A., Gao, J., ter, P., Frantz, P., Gabisi, A., Gall, R., Gorrell, J.H., Guev, Hamilton, K., Han, J., Harris, C., Harrwes, A., Hernandez, J., Harris, C., Han, J., Kovat, C., Liu, Y., S., Hume, J., Ioshikhes, I., Jacks Ohnson, R., Jolivet, S., Joudah, S., Lewis, J., Lichtarge, O., Lieu, C., Liu, J., Liu, J., Lu, X., Lucier, A., Lucier, R., Lun, J., Marsey, E., Mawhiney, E., McLeod, S., E., Massey, E., Mawhiney, E., McLeod, Scher, S., Watcher, M., Miller, A., Mine, Mohabbat, K., Montgomery, K.T., Morgan al, D., Nelsenson, E., Nockenko, S., Payto ters, L., Pickens, R., Primus, E., Pu, L., Ler, J., Dess, A., Rojubokan, I., Solie, B., Sodergren, E., Sonaike, T., Sparka, Sutton, A., Saparka, Sutton, A., Saparka, Tabor, P., Tamer Tansey, J., Taylor, C., Taylor, T., Telf Usmani, K., Vasquez, L., Vera, V., Villang, S., Ward-Moore, S., Warren, R., Morley, K., Wu, C., Wu, Y. F., Zhati, R., and Gibbs, R.	a; Chordata; Craniata; vertebrata; Eute a; Euarchontoglires; Primates; Catarrhi 8785) C., Adio-Oduola,B., Ali-osman,F.R., Al maratunge,H.C., Are,J.R., Banks,T., Bar M., K., Blankenburg,K., Bonnin,D., Bouck,J M., Brown,E., Brown,M. Bryant,N.P., Bu M., Brown,E., Brown,M. Stryant,N.P., Bu ,C., Burrell,K.L., Byrd,N.C., Carron,T.	158785 bp DNA linear ns 12 BAC RP11-179A1 (Roswell Park Cancer y) complete sequence. 8 GI:13899365 ns (human)

REFERENCE AUTHORS TITLE REFERENCE TITLE JOURNAL AUTHORS JOURNAL Submitted (25-UJL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 158785) Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 158785) Direct Submission

COMMENT

JOURNAL

Worley, K.C

Direct Submission

Submitted (19-MAR-2003) Human Genome Sequencing Center, Dep Submitted (19-MAR-2003) Human Genetics, Baylor College of Medicine of Molecular and Human Genetics, Baylor College of Medicine Baylor Plaza, Houston, TX 77030, USA

On May 1, 2001 this sequence version replaced gi:13877202.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu Center, Depar of Medicine, Department

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. only of

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality strandards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT------

Position 10464 10467 10469 10491 10511 13930 Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus: Phrap values in estimate: Contig length: Original+Context
ctttctc(n)ttntntctct
tcttctcnt(n)tntntctct
tcttctcnttnt(n)tctctctct
tcttccnttnt(n)tctctctct
tctttcccta(n)tctcctct
tctttcccta(n)tcncctcct
taccccactc(n)ntnnnncaag Consensus changing edits Summary Statistics Edited+Context 158572 4.46022e-06 0.00425044 30 158785

taccccactc (c) ctgcaacaag

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FEATURES
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CTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATG 222
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/clone="""
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                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                    /clone="RP11-179A1"
                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
(mol_type="genomic DNA"
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acagcaagan (n) aacaaagctt
tggagtgcag (n) ggacacaatct
gtatttttag (n) agagacggag
ctttcagaga (a) t. . . .
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tatgactaag (n) gaagtttacc
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AC133054
AC133054.2 GI:22213530
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Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 174874)
McPherson, J.D. and Waterston, R.H.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
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Submitted (29-MAY-2002) Genome Sequencing Center,
C+ Louis. MO 63108, USA
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McPherson, J.D. and Waterston, R.H.
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                                                                                                        Submitted (05-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Aug 13, 2002 this sequence version replaced gi:21217626.
                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                        Direct Submission
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                                            Center: Washington University Genome Sequencing Center Center code: WUGSC Web site: http://genome.wustl.edu
              Contact: submissions@watson.wustl.
Center project name: M_BB0220N11
                                                                                                                                                                                                         (13-AUG-2002) Genome Sequencing Center, St. Louis, MO 63108, USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

밁 Ś 밁 8 밁 S

C-TCATAAACAAACAATGAGAGTTTTCTTTTATTGATGCTTTACTTCACTGCTACACTTT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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This sequence is the entire insert of the clone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
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11394
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Glires; Rodentia;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Murodea; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                             Bielicki, L.

The sequence of Mus musculus
Unpublished (2001)
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               Submitted (11-NOV-2003)
                                                                                    Submitted (29-JAN-2003)
                                                                                                Direct Submission
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McPherson, J.D. and Waterston, R.H.
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University, 4444 Forest
                            Direct Submission
                                        Wilson, R.
                                                                      Parkway, St.
                                                                                                               McPherson, J.D. and Waterston, R.H.
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                                                                     63108,
Department of Genetics,
Park Avenue, St. Louis,
                                                                      Genome Sequencing 63108, USA
                                                                                                                                             Genome Sequencing 63108, USA
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Washington
Missouri 63108,
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COMMENT
NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                    On Jan 29, 2003 this sequence version replaced gi:25450603
                                                                                                                                                                                                                                          Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl
Contact: Summary Statistics
                                                                                                                                                                                                                 Center project name:
                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                 M_BA0480E08
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu

SOURCE INFORMATION:
The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Greatlanned by CC13064 This clone is

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2 (bases 1 to 196859)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehotz, K., Matthews, C., McCathy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H.,
                                                                                                                                                                                                                                                     Hominidae; Homo.
1 (bases 1 to 196859)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-514F3
                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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51765. .51952
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REFERENCE AUTHORS

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O'Connor,T., O'Donnall,P., O'Wall,D., Oliver,J., Petersen,K., Phunkhang,P., Pietre,N., Follara,V., Raymond,C., Retch.R., Rishock,M., Rilby,R., Rishock,M., Raymond,C., Raymond
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Center clone name: 514_F_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="Alusg"
complement(1696..20
/rpt_family="MLT1F1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2441. .2542)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-11 Human complement (1362. .1667)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="L1MC4a"
complement(2895..32)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type= 5----9606"
/db_xref="taxon:9606"
 /rpt_family="FLAM_A" complement(16491...1
                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (5971. .6301)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="L1MC4a"
4703. .4723
                                                                                                                                                                                                                                                                            complement (11082. .11330)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                   complement(9716. .10072)
/rpt_family="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (5756)
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. 3995
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ement (con:
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                                                                                                                                                                                                                             family="MIR"
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ement(11000)
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                                       family="AluSx"
                                                                                                                                                                                                                                                                                                                                                             family="MIR3"
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                                                                                                                                   .3852
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                                                                                                                     y="MER58"
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.16704)
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AC124696
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                                                                                                                                                                                                                                                                                                 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                                                                                          AC124696 193849 bp DNA linear HTG 29-APR-2005 Mus musculus chromosome 16 clone RP24-173I13, WORKING DRAFT SEQUENCE, 8 unordered pieces.
AC124696 AC124696.4 GI:62955023
                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                ATATATTTATATAAATATATATTATATACTTATATATTTATATATTT 146334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTGAGAGGTATTTTAACACACCTTAGAACTAAAACTTAATAATAATAATATTTCTCTAT 162
                                                                                                                                                                                                                                                                                                                                                                          AAATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTTGTCTTTTGCTTCTCTAAAGGTC 402
                                                                                                                                                                                                                                                                                                                                                                                                                                               CTATTTATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATATAATAATATATATAATATATATATATATATATATCAAATAAATATATATATATATAA 146046
                                                                                                                                                                                                                                                                                                 TTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTT 450
                                                                                                                                                                                                                                                                                                                                     TCGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(16710...17026)
/rpt_family="AluJo"
complement(17031...17250)
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complement(22225. .22279)
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20431.
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ement (21)
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0; Mismatches 223;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson,R.K.
Direct Submission
Submitted (29-APR-2005) Genome Sequencing Center, 4444 Fore
Parkway, St. Louis, MO 63108, USA
On Apr 29, 2005 this sequence version replaced gi:24416033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 193849)
McPherson, J.D. and Wat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sciurognathi; Muroidea; Muridae; Mus. 1 (bases 1 to 193849)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-JUN-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkway, St. Louis, MO 3 (bases 1 to 193849)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: M_BB0173I13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1053
1153
2248
2348
3389
3489
                                                                                                                                                                                                                                                                                                                                                                                                              4997
                                    /estimated_length=unknown
1153. .2247
/note="assembly_name:Contig30"
                                                                                                                                                                                                                                                              Location,
   'estimated_length=unknown
                                                                                                             note="assembly_name:Contig23"
                                                                                                                                                  /clone="RP24-173I13"
                                                                                                                                                                       chromosome="16"
                                                                                                                                                                                     /mol_type="genomic DNA
/db_xref="taxon:10090"
                                                                                                                                                                                                                           organism="Mus musculus"
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                                                                                                                                                                                                                                            .193849
                                                                                                                                                                                                                                                                               80358: gap of
193849: contig
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1152: gap of unknown length
2247: contig of 1095 bp in length
                                                                                                                                                                                                                                                                'Qualifiers
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contig of 1041 k
gap of unknown l
contig of 1508 l
gap of unknown contig of 1527 l
gap of unknown contig of 1527 l
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SOURCE KEYWORDS

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NuznyD. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
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Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
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Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L.,
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Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
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Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K.,
Harvor, V., Hamilton, K., Hamilton, K.,
Harvara, V., Hamilton, K., Hamilton, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84641 ATGTATGTACACATCGCAGATGGAGTTTACAATTTGAGCTGACA 84684
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
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Bos taurus clone CH240-125K20, ***
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pecora; Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT
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4997. .5096
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80359. .193849
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3389. .3488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA linear HTG 01-JUL-2005
SEQUENCING IN PROGRESS ***, 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 193849;
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

Center project name: FHXA
Center clone name: CH240-125K20
Center clone name: CH240-125K20
Center clone name: CH240-125K20
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 239556 bases at least Q40
Consensus quality: 233265 bases at least Q20
Consensus quality: 236194 bases at least Q20
Bstimated insert size: 239301; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ----- Project Information

Project Information

Center code: BCM

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Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, R.,
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Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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Maniney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Mangran, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
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Nankervis, C., Neal, D., Newton, N., Muypen, N., Norris, S.,
Plopper, F., Poindexter, A., Perez, A., Perez, L., Pfannkoch, C.,
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Plazo, M., Quiroz, J., Rachlin, B., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Wang, O., Wang, S., Warren, J., Walter, B., Wang, J.,
Wang, O., Wang, S., Warren, R., Welk, A., Tabor, P., Taylor, C.,
Wang, G., Willson, R., Wuc, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, S., Yen, J., Yoon, L., Yoon, V.,
Willasana, D., Warren, R., Wels, S., Wente, F.,
Weinstock, G. and Gibbs, R.A.
                                                                                                                               of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 29, 2005 this sequence version replaced gi:67514619.
On Jun 29, 2005 this sequence version replaced gi:67514619.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.ttmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-dUN-2005) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 244638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
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Center: Baylor College of Medicine
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gap of 50 L

J14: contig of 11

38.90: gap of 676 bp

55.38: gap of 50 bp

76.34: gap of 489 bp

76.34: gap of 489 bp

76.34: gap of 489 bp

76.34: gap of 50 bp

83.875: contig of 7481 bp in leng

83.876: gap of 50 bp

94.35: gap of 50 bp

94.35: gap of 10209 bp in length

94.35: gap of 3517 bp in length

97.85: gap of 3517 bp in length

97.85: gap of 50 bp

97.85: gap of 559 bp

108.59: contig of 108.5 bp in length

108.70: length 559 bp

115.82: contig of 5543 bp in 1

121.55: gap of 50 bp

131.73: contig of 50 bp

131.73: gap of 50 bp

132.8: gap of 50 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
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209272
209372
209372
211085
211135
221593
220593
220643
223228
2233228
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195601
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151083
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12739
16582
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189402:
195600:
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181887:
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151032:
151082:
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12688: contig of 3944 b
12738: gap of 50 bp
16591: contig of 3843 b
16631: gap of 50 bp
22198: contig of 5567 b
                  contig
gap of
contig
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contig
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g of 8305 bp in length
of unknown length
ig of 10904 bp in length
                                              unknown
of 1127
                    unknown
of 1587
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of 1713 bp
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Best Local Sim
Matches 152;
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                                                          76676 ATACATNAAANTTANAATTTNNNTNATNNNNANNNTATTTNNNTAAATTNNNNTTAATTT
                                                                                                                                                                                                                                           76616 AAATANTTNAATAAANATNAAATTNTNTTTATACATTAAAATTTAATATATAAANNTAAA 76675
                                                                                                                                                                                                                                                                                                       76496 AAATTTTATAAATTTATATTATAAAAANTTNANATTTTNAAAAATTTTTATATAAATATT
                      399 GGTCTTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTTGCTTT
                                                                                                                                                 279 GCCACTATTTATCTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTGGCC
                                                                                                                                                                                                             219 CATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATAT
                                                                                                                                                                                                                                                                        159 CTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACT
                                                                                                                                                                                                                                                                                                                                    99 ATTTATTTGAGAGGTATTTTAACACACCTTAGAACTTAAAACTTAATAATATATTTCT 158
                                                                                                                                                                                                                                                                                                                                                                                                39 ACAGTATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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235006
235106
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236776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Bos taurus"
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/db_xref="taxon:9913"
/clone="CH240-125K20"
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231472: contig of 165 b
231572: gap of unknown 1
233019: contig of 1497 b
233119: gap of unknown 1
235105: gap of unknown 1
235105: gap of unknown 1
236675: contig of 1570 b
236775: gap of unknown 1
236471: gap of unknown 1
244371: contig of 3596 b
244471: gap of unknown 1
244638: contig of 4167 b
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Aba61080 Human gen
Abg66998 Human ang
Abj13236 Human imm
Abg15253 Oligonucl
Acil3336 Rice stre
Ad271063 Human chr
Abv99761 Human pfx
Abs46704 Tumour su
Abi33929 Human imm
Abj13291 Chemicall
Abl49362 Human pol
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Abs77246 DNA segue
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ALIGNMENTS

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RESULT 1
ADO39580
Heterologous gene; expression cassette; gene expression; yeast; CALL; gene; ds.
                                                                                       Wilkinson JQ, Mcbride
                                                                                                                                         20-JUN-2003; 2003US-00600230
                                                                                                                                                       13-MAY-2004.
                                                                                                                                                                                Saccharomyces cerevisiae.
                                                                                                                                                                                            gene;
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                                                                          WPI; 2004-374960/35.
                                                                                                                             20-JUN-2002; 2002US-0390529P
                                                                                                                                                                   US2004092020-A1
                                                                                                   (WILK/) WILKINSON J
(MCBR/) MCBRIDE K.
(BERT/) BERTAIN S.
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                               -termination DNA.
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The present invention relates to heterologous genes comprising non-plant 3'-termination sequences and plant expression cassettes incorporating the heterologus genes. The invention is useful for gene expression in plant cells. The present sequence is yeast CALI 3'-termination DNA. This sequence is used in the invention.

New recombinant expression cassette comprising a promoter that functional in plants, operably linked with a coding sequence an plant 3' termination sequence, useful for gene expression in pl

at is and a plant

noncells.

Claim 4; SEQ ID NO 1; 74pp; English.

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RESULT 2
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XX AD03
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            Wilkinson JQ,
                                                                                                                                                      US2004092020-A1
                                                                                                                                                                             Saccharomyces cerevisiae
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                                   (WILK/) WILKINSON J
(MCBR/) MCBRIDE K.
(BERT/) BERTAIN S.
                                                                                 20-JUN-2002; 2002US-0390529P
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AC Huma
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Matches 476;
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                                                Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; phihalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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GENBANK; X57300.
                            neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                            ABL32718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL32718 standard;
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Pred. No. 1.2e-101;
D; Mismatches 2;
                                                                                                                                                                                                                                                                               gene
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                CCGAATATGCCACTATTTATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTG
                                                                                                                                                                                                                        GTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACT
                                                                                                                                                                                                                                                                                        ATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACT
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                                                                                                             TCTCTAAAGGTCTTCAATTTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTT
                                                                                                                                TTTTATATAAATTTTTTTGTTAGTTATTTTTTTTTGTGTACGTTTTAAAAATGTTTGTATG
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llarity 45.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 46.2; DE Pred. No. 0.5; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; 1217 G; 3027 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                  The invention relates to 224 nucleic acid sequences comprising at least CC 18 bases of a chemically pretreated gene associated with gene regulation CC selected from 43 known genes (or complementary sequences). The chemical CC pretreatment converts cytosine bases unmethylated at the 5-position to convert converts cytosine bases unmethylated at the 5-position to CC cytosine, to enable analysis of cytosine methylations. The DNA sequences, CC oligomers (or sets/arrays) and method are useful in the diagnosis of CC diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are cepecially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this patent did not form part of the complete control of the cytosiated specification and is associated with the human gene regulation-associated control of the cytosiated specification, but was obtained in electronic format directly into the cytosiated control of cytosiated control of cytosiated control of cytosiated cytosiated control of cytosiated c
                                                                                   Query Match
Best Local S
Matches 181
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analyzing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency disease.
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                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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  regulation-associated
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nilarity 46.8%;
Conservative
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; 2000DE-01032529.
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RAG ABG6
RAG
The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of anglogenesis-associated genes (II) having sequences (ABG6671-ABG67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human angiogenesis associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid fragments from chemically treated angiogenesis-
associated genes, useful for determining methylation status, e.g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis; methylation; eye disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37515 BP; 11428 A; 425 C; 7165 G; 18497 T; 0 U; 0 Other;
The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular plaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                             30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune system associated
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                                                                                                                                                                                                                                                                                                                                                     WO200200928-A2
                                                                                                         Claim 1; SEQ ID NO 309;
                                                                                                                                             diagnosis and treatment
                                                                                                                                                        Nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA; 7201
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                                                                                                                                                                                                            Piepenbrock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system disease; cytosine methylation;
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Pred. No. 1.
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                                                                                                                                             chemically modified gene, useful associated with abnormal cytosine
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RESULT 7
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This invention describes a novel method for determining the degree of comethylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligomaclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of collgomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases.
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                                                                                                                                                                                                                                                                     Determining the degree of cytosine methylation in genomic DNA, useful diagnosis and prognosis, comprises selective hybridization of amplicon
                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-2000; 2000DE-01043826
05-SEP-2000; 2000DE-01044543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide
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                                                                                                                                                                                                                           Sequence Listing; 56pp;
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Pred. No. 1.1;
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Best Local S
Matches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disclosure of the invention
 Oligonucleotide
                       12-JUL-2002
                                                                  ABQ15252 standard; DNA; 517
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                                                                                                                                             TCAATTTATCTAAAGCAAGTTTTGTATAAT
                                                                                                                                                                                                                                  TATTTATCTGTGGCATTTCCCAATTTATATTCCCCCTATTGGGTATTTGATGTGGCCGTTTA
                                                                                                                                                                                                                                                                              CGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCAC
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detecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44.4;
Pred. No. 0.
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 cytosine methylation
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RESULT 8
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ID ABQ1
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KW Huma
KW Gast
KW G
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                                                                                                                                                                                                                                                                                    01-SEP-2000; 2000DE-01043826
05-SEP-2000; 2000DE-01044543
    WPI; 2002-371829/40
                                                                                             Olek A,
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Best Local Sim:
Matches 174;
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                                               Rice stress-regulated promoter
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                                               SEQ
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Matches 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-2001;
26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; abiotic stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-248011/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kreps J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SYGN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                               309
                                                                                                                                                                                                                                                                    313
                                                                                                                                   193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; SEQ
                                                                                                                                                                                                                                                                                                   69
73
                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                   YYSWAAWKGWWRWSKTTWARRWSWAWRWKTWAKWYRAAYSKWKKKWWYWTRAAWMATRMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000
                               ATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAA
                                                                                                TTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAATTT 308
                                                                                                                                                                                                                                                                                                   TACAAGTTGATATATGGTTGTGTGTAACTTATTTTGAGAGGTATTTTAACACACCTT
                                                                                                                                                                                                                                                                                                                                    AAGGAAGTCGTTTAGSWCMWTKTWWMWKTMRMWMKTKKAWAKAWAWAYYMYSMRYRWMY 314
                                                                                                                                                                                                                                                                                                                                                                  AAGGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTTACTGTGATACT
MSGSAGYMTKYAKYWMMTRWKTRKTKRTSWKAWWM
                                                                 GTMWWWRKYAWSWTWTKKRKWYMWKRTMRYWKYCCKRAWMSWCYTKSWWWWYKMSTWSKR
                                                                                                                                   AKWYWTKYWTWRRAGWMYRYRTMKMTSWCYTWWMMRWMWWYWTTTWYRWRKAMRKARGRA
                                                                                                                                                                AGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCG
                                                                                                                                                                                                    TWMMTWWWARKWTRYWWAKWTYAMWWTKYAAWAAWTATWTKWATRGAWWTRWSWAGWMAA
                                                                                                                                                                                                                                  AGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTA
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T, Provart N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2001US-0300112P.
; 2001US-0314662P.
; 2001US-0325277P.
; 2001US-0332132P.
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002WO-US019668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 540 A; 344 C; 416 G; 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO 13926; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cooper B,
                                                                                                                                                                                                                                                                                                                                                                                                      147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricke D,
                                                                                                                                                                                                                                                                                                                                                                                                  Score 43.6; DB
Pred. No. 1.7;
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glazebrook J,
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for altering the an abiotic stress such as
                                                                                                                                                                                                                                                                                                                                                                                                      146;
                                344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goff SA,
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Katagiri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid
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Matches 55
                                                                                                                                                                                                                                                                                                                     The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, sentice stress or any of their combinations. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-2001; 2001US-0300112P.
24-AUG-2001; 2001US-0314662P.
26-SEP-2001; 2001US-033277P.
21-NOV-2001; 2001US-0332132P.
                                                                                                                                                                                                                                                                        Sequence 2000 BP; 510 A; 350 C; 268 G; 518 T; 0 U; 354 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 48; SEQ ID NO 15671; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003008540-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ss; abiotic agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rice stress-regulated promoter SEQ ID NO:15671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACL37108 standard; cDNA; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-2002; 2002WO-US019668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                      451
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                                                                                                                                                                        9
                                                                                                                                                                                                        55;
                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                           in the exemplification of the invention
                                                                                    TACAAGTIGATATATGGTTGTGTAACTTA--TTTATTTGAGAGGGTATTTTAACACACCC
: |:::: : |::: :: ::|
KGTRRYYYRMKRAAYWTRWMATRSATWCTGWTYWTSAKTTKWKRWAGYAKATTMKMRKTY
                                TTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTAAAGGCACATATTACGTGGC
                                                                                                                                    ARKAWGKARWAYCKRTTAYATMTTTTRRTRAAWWMYTGMRKRRSMTRWRMTSRWTTWSW
                                                                                                                                                                  AAGGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACT
                                                                YKWYYYWTRRYRASRARTKGKATKYTMTWKWMMGCWSYTKARWWMMAYKKSWKMAWYAWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Briggs SP, Cooper B, G
T, Provart N, Ricke D,
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stress tolerance; transgenic plant; plant; cereal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                      8.9%;
                                                                                                                                                                                                      206;
                                                                                                                                                                                                 Score 43; DB 11; L
Pred. No. 2.3;
6; Mismatches 186;
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D, Zhu T;
                                                                                                                                                                                                                                      DB 11; Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for altering the an abiotic stress such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goff
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Katagiri
                                                                                                                                                                                                    4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               片
                                        The invention relates to a purified and isolated DNA sequence having protein production increasing activity comprising at least one bent DN element, and at least one binding site for a DNA binding protein. The purified and isolated DNA sequence comprising a first and a second isolated matrix attachment region (MAR) nucleotide sequence, which is MAR nucleotide sequence selected from a purified and isolated DNA sequence above, a purified and isolated MAR DNA above, a purified and isolated clyMAR element and/or fragment, a synthetic MAR sequence, a sequence complementary to it, its molecular chimera, or its combinatio and variants, is useful for increasing protein production activity in eukaryotic host cell. The present sequence represents a human chromoso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L063/c
ADZ71063
                                                                                                                                                                                                                                                                                    New purified and isolated DNA sequence having protein production increasing activity comprises a bent DNA element and a binding site for DNA binding protein, useful for increasing protein production activity is eukaryotic host cell.
                                                                                                                                                                                                                                                                                                                                                                                                         Mermod N,
Puttini S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; matrix attachment region; MAR; protein production
                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 187; 282pp; English.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-333507/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-OCT-2003;
06-FEB-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-2004; 2004WO-EP011974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human chromosome 2 contig DNA SEQ ID NO 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SELE-) SELEXIS SA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGTATAATTCAAAATACTTTGCTTTTCTCC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYWTTWMWMRCRAGWWWKGGMAKRAAARTKWMRTYRMKKMWRYRWYKWSWARGWRAWRKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAGGRWWYKKWASSRTWKWCWYKMYMWATKKSWWSWATTWAWKSMWYKKKWTYYTYMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRKTSYYYTKKWWKKMWSSGYYWRYYTTTMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRCRTRWKGWTRWKTWKMWRWYKKRTYRMKKSAKWWYMRSGAYRRRWMRRMAYSRRRSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCTTCAATTTATCTAAAGCAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYTYWWYMMYRCAWMWYSAYWRSWRRWTTTKYSKMYYWKMWMRRTYARAKAYSRWWMWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACT--ATTTATCTGTGGCATTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACG
                                                                                                                                                                                                                                                                                                                                                                                                                        Girod PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2003US-0513574P.
2004EP-00002722.
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Sequence 847 BP; 501 A; 17 C;

10 G; 319

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0 U; 0 Other

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 PRESENTATION OF THE PROPERTY O
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ABV99761/c
ID ABV99761 standard; DNA; 22617 BP.
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Best Local S
Matches 186
                                                                                                                                                                                                                                                                                                                                                        Human; 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2; PFKFB2; cytostatic; antidiabetic; gene therapy; cancer; diabetes; SNP; gene; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human PFKFB2 gene.
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                                                                                                                                                                                                                                                                                        Location/Qualifiers replace(1342,G)
                                                                                                                                                                                                                                              /standard name= "Single nucleotide polymorphism"
replace(1366,T)
              replace(10169,A)
/*tag= g
                                                                                                                                                                                                         /standard_name= "Single
replace(1686,A)
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                standard_name=
132. .20748
                                           number= 1
                                                                   217. .10307
                                                                                 number= 1
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                                                                                                                                        product= "PFKFB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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Pred. No. 2.8;
                                                                                                                                                                                "Single
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                                                                                                                           introns"
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/*tag= n
/number-
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/*tag= i
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/*tag= h
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/number= 6
12186. .13405
/*tag= t
/number= 6
13406. .13530
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                                                                                                                                                                                                                                                                                                                                                                              /number= 7
15873. .16080
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                                                                                                                                                                                                            /number= 9
17799. 17903
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16686. .17798
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/number= 8
16539. .16685
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16081. .16538
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11073. .11498
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.0976. .11072
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/number= 7
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1566. .11702
     /*tag= ac
/standard name= "Single nucleotide polymorphism"
18558. .18787
/*tag= ae
/number= 11
18788. .19565
                                                                                                                                                                      replace (17839,
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*tag= v
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                                                                                         eplace (17911, A)
                                                                                                        number=
                                                                                                                              standard_name= "Single nucleotide polymorphism" 7904. .18657
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                                                                                                                                                         Sequence 22617 BP; 5587 A; 4922 C; 5366 G; 6741 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                             Example 1; Fig 1; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                Duda A,
                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2000; 2000US-0209935P
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                                                                                                              l Similarity 77; Conser
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  CTTTAAAGGCACATA 177
                                            TATATAAAGATATATAAATATATATAAAGATATATATAAAGATATATATAAAATATAT
                        Conservative
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/number= 11
19566. .19628
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replace(21098,G)
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/*tag= ak
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57.0%;
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                                                                                                             Score 42.2; DB Pred. No. 5.5; 0; Mismatches
                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleotide polymorphism
                                                                                                                                    DB 6;
                                                                                                              58;
                                                                                                                                  Length
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                        9416
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S

43 TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT 102

Matches Query Match Best Local S

Similarity

8.7**%**; 56.5**%**;

Conservative

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Length 14615; Indels

Score 42; DB 4; Pred. No. 5.6; 0; Mismatches 6

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ARAS46
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ANC CYCOS
ANX Human
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                                                                                                   The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and oncogenes CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and CC 500 are missing from the sequence listing) sequences (Ss) and sequences CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of CC probes for detecting the cytosine methylation state and/or single CC nucleotide polymorphisms and also to be used in an array for analysing CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The probases can also be used in a method for ascertaining genetic and/or cytosine methylations. The parameters may be compared to another set of CC genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to CC patients. The present sequence is one of the 533 genomic sequences CC derived from tumour suppressor genes and oncogenes. Note: The sequence color of this patent did not form part of the printed specification, but CC from winc, introduction of the compared to action, but CC control of the control of the control of the sequence color of the control of the control of the sequence color of the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
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06-APR-2000; 2000DE-01019058
07-APR-2000; 2000DE-01019173
30-JUN-2000; 2000DE-01032529
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    Sequence 14615 BP;
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4072 A; 253 C; 3233 G; 7057 T; 0 U; 0 Other
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Matches 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL33929
                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
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                                             The present sequence is a gene of the invention
                                                                                                Conservative
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rheumatoid arthritis; psoriasis; bowel dis
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                                                                                           Score 41.6; DE Pred. No. 6.1; 0; Mismatches
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5417
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RESULT 15
ABL92291
ABL92291
                                                                                                                  New nucleic acid derived from genes associated with DNA repair, for diagnosis, e.g. of ataxia telangiectasia, by determination cytosine methylation.
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                                                                                                                                                                                                                                        30-JUN-2000;
01-SEP-2000;
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07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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Nijmegen breakage syndrome; Werner syndrome; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA repair; cytosine methylation; PMS2L1; PMS2L12; IL4; PMS2L5; PMS2L6; MGMT; MSH2; NUDT1; TDG; INPPL1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemically treated
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                                                                                           Claim 1; SEQ ID NO 100;
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2000DE-01019173.
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2000DE-01043826.
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DT1; TDG; INPPL1; RFC4; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment complementary to#50
                                                                                                                                                                                                                                                                                                                                                                                                  solid tumour; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Cockayne syndrome;
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DDIT1L; FANCB;
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acids comprising at least 18 base pairs of the chemically of genes associated with DNA repair selected from PMS2L1, PMS2L2, PMS2L3, PMS2L4, PMS2L5, PMS2L6, MGMT, MSH2, NUDT RFC4, DDIT1L, FANCB, or XRCC8. Nucleic acids of the invent

acids of the invention and

related INPPL1,

NUDT1,

The invention relates to nucleic acids containing a sequence of at least 18 nucleotides of chemically treated DNA of genes associated with DNA repair, and their complements. The invention also relates to nucleic acids comprising at least 18 base pairs of the Chemically pretreated DNA of genes associated with DNA repair selected from PMS2L1, PMS2L12,

Query Match 8.6%; Score 41.6; DB 6; Length 6801; Best Local Similarity 44.1%; Pred. No. 6.1; Matches 173; Conservative 0; Mismatches 219; Indels 0; oligomers, are useful for diagnosis of diseases associated with gene repair, specifically ataxia telangiectasia, aging, Bloom's syndrome, Cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome, immunodeficiency, trichthiodystrophy, Fanconi's anaemia, solid tumours and cancer, particularly by determining status of cytosine methylation and/or by detecting single-nucleotide polymorphisms. Determination of individual methylation patterns may allow development of individualised therapies. The sequences given in records ABL92192-ABL92335 represent chemically pre-treated DNA fragments from genes associated with DNA repair, and their complements. Note: The sequence data for this patent is not represented in the specification, but is based on sequence information supplied by the European Patent Office Sequence 6801 BP; 2041 A; 163 C; 1563 G; 3034 T; 0 U; 0 Other; 5658 TTTTTTTTTTTTCGGTTTCGTTTTTTTATTTTTATTTTGGTTTTTAATTTT 5418 TTTAATAATAGAAAGATAATTTAATTTAAAAATGAGTAAGGGATTTAAATTGATATTTTT 5477 420 AAGTTTTGTATAATTCAAAATACTTTGCTTTT 451 360 ATCTTCACTTGTTCGAGTTTTTGTCTTTTTGCTTCTAAAGGTCTTCAATTTATCTAAAGC 419 300 TTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGA 359 240 TAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCAT 180 ACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTC 239 120 ACACACCTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATT 179 60 TGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTTTATTTTGAGAGGGTATTTTA 119 Gaps 299

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Search completed: December 28, 2005, 09:24:31 Job time : 499 secs

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Result
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Copyright (c) 1993 - 2005 Compugen Ltd.
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   9 BZ302050
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AL063721 Drosophil
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ALIGNMENTS

Q Q	Query Match Best Local : Matches 16:	ORIGIN						source	FEATURES						COMMENT	PUBMED	JOURNAL	TITLE	AITHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	RESULT 1
195 TTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGT 254	Match 13.8%; Score 66.8; DB 9; Length 495; Local Similarity 56.5%; Pred. No. 7.1e-05; es 166; Conservative 0; Mismatches 122; Indels 6; Gaps 2;		<pre>/clone_lib="Kluyveromyces delphensis Random Genomic Library"</pre>	/clone="KD1625"	/db xref="taxon:51657"	/mol_type="genomic DNA" /strain="CBS 2170"	sm="Kluyvero	1495		Class: plasmid ends.	Fax: 353 1 6798558	353 1	Dublin 2, Ireland		Contact: Wong S	12620120	Genome Biol. 4 (2), R10 (2003)		Wong S. Fares M.A. Zimmermann W. Butler G. and Wolfe K.H.	Saccharomycecares; Saccharomycecaceae; Ninyveromyces. 1 (bases 1 to 495)	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	Kluyveromyces delphensis	Kluyveromyces delphensis	GSS.	BZ302050.1 GI:24448520	BEZ302050	Kluyveromyces delphensis genomic clone KD1625, genomic survey	1 Kluyveromyces delphensis Random Genomic Li	BZ302050 495 bp DNA linear GSS 31-OCT-2002	

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82 TCAAATTTCATAGACAGTAAAACTTAGGGACCCATTAAATTTCTCCAGCACTCTTTCTGT 141

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AUTHORS
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1001)
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AL062781
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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  GGTATTTTAACACACCTTAGAACTAAAACTTAATAAATATTTTCTCTATCTTTTAAAG 170
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                                                                                                                                                                                                                                                                                 /clone="BACR13009"
/clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:7227"
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                                                                                                                                                              Mismatches
<del>--</del>
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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AL063921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCGATTGAATCTTCACTTGTTCGAGTTTTTGTCTTTTTGCTTCTAAAGGTCTTCAATTT 410
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                                                                                                                     /clone="BACR08K10"
/clone_lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                    /mol_type="genomic DI
/db_xref="taxon:7227
                                                                                                                                                                                                                                                      organism="Drosophila melanogaster"
                    10.7%; Score 51.8; D
15.6%; Pred. No. 0.2;
181;
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  Mismatches
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survey sequence TET3 end of BAC #
rom Drosophila melanogaster (fruit
                                                 DB 10;
  154;
  Indels
                                                 Length 1101;
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43 TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTAACTTATTT 102

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                                                                                                                                                                                     source
                                                                                                                                                                                                                            - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Concer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence.
AL069706
AL069706.1 GI:4949849
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (fruit fly)
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                                                                              /mol_type="yearch.../db_xref="taxon:7227"
                                                                                                                                                                                                           Location/Qualifiers
                           /clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                        organism="Drosophila melanogaster"
|mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                  1 (bases 1 to 1191), Kremitzki, C., Carter, J., McPherson, J., Warren, W., Mardis, E. and Wilson, R.
A physical map of the xenopus tropicalis genome Unpublished (2003)
                                                                                                                                                                                Email: submissions@watson.wustl.edu
Insert Length: 75000 Std Error: 0
Seq primer: T7 TAATACGACTCACTATAGGG
Class: BAC ends
                                                                                                                                                                                                                                           Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                          Contact: Richard K Wilson
                                                                                                                                                                                                                                                                                                                                                                Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus tropicalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic survey sequence.
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                                                                                                                                                                  High quality sequence start:
                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus tropicalis (western clawed frog)
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                                                                                                                                    quality sequence stop: (
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                                                                      organism="Xenopus tropicalis"

mol_type="genomic DNA"

db_xref="taxon:8364"
              /clone_lib="ISB1"
/note="Vector: pBeloBAC11;
Library Segment 1"
                                                          clone="ISB1-43I12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:40598380
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tropicalis genomic clone ISB1-43I12,
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                              ISB-1 Xenopus tropicalis
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Query Match Best Local Similarity

9.9%;

Score 47.8; DB Pred. No. 1.6;

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RESULT 6
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BH945927
BH945927.1
GSS.
                                                                                                                                                                                                                                Seq primer: -21UPpOT forward Class: shotgun
                                                                                                                                                                                                                                                                                                                  Whole genome shotgun reads from Brassica oleracea Unpublished (2002)
Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH945927 7
obu88a02.b1 B.oleracea002
                                                                                                                                                                                                                                                             Email: submissions@watson.wustl.
Plate: obu88 row: a column: 02
                                                                                                                                                                                                                                                                                       Genome Sequencing Center Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                            Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
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                                 /note=TVector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TOLOODHA buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                        Sequencing Center.
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                                                                                                                     lib="B.oleracea002"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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AL098595
AL098595.1 GI:5610206
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                        organism="Drosophila melanogaster"/
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                                                                                  clone="BACN03K20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS016LI 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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AL106896.1 GI:5624374
                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                         : www.genoscope.cns.fr)
/clone lib="DrosBAC"
/plasmId="pBeloBAC11"
/note="end : T7"
                                                                                  /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                 Location/Qualifiers
                                                                 /clone="BACN16D22"
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2; Mismatches 171;
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Best Local Similarity
Matches 103; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildae; Drosophila.

1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                   - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genome sum
BACN37D10 of DrosBAC library from
fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                       d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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9.5%; Score 46.2; ilarity 14.7%; Pred. No. 3 Conservative 170; Mismatch
                                                                                                             /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                      /mol_type="genomic DN/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                 clone="BACN37D10"
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and of BAC
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The genome of the host-cell transforming parasite Theileria annulata and a comparison with T. parva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ929051 GI:67499440
EST
                                                                                                                                                                                                                                      The Wellcome Library NITED KINGDOM
Genome Campus, CB10 18A, UNITED KINGDOM
Merozoite cDNA library: Frank Katzer and Brian Shiels, Division of
Merozoite cDNA library and Immunity, ICM, University of Glasgow, UK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pain, A., Renauld, H., Berriman, M., Murphy, L., Yeats, C.A., Weir, W., Kerhornou, A., Aslett, M., Bishop, R., Bouchier, C., Cochet, M., Coulson, R. M.R., Cronin, A., de Villiers, E., Fraser, A., Fosker, N., Gardner, M., Goble, A., Griffiths-Jones, S., Harris, D.E., Katzer, F., Gardner, M., Goble, A., Griffiths-Jones, S., Harris, D.E., Katzer, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ929051 Theileria annulata merozoite Theileria annulata cDNA clone tam024c03_q1k, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2005)
Contact: Pain A
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Theileria annulata
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                                                                                                                                                                                                                             Veterinary Infection and Immunity,
Location/Qualifiers
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1 (bases 1 to 1161)
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                                                                                                                                                                                                                                                                                                                    Pathogen Sequencing Unit Wellcome Trust Sanger Institute
/clone="tam024c03_q1k"
/dev stage="merozoite"
/lab_host="Bos taurus (cow)"
/clone llb="Theileria annulata merozoite"
/note="country: Turkey:Ankara"
                                                                                                              /isoTate="Ankara (clone D7)"
/db_xref="taxon:5874"
                                                                                                                                                                                  organism="Theileria annulata"
                                                                                                                                                             type="mRNA"
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Best Local Similarity
Matches 171; Conserv
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                                                                                                                                                                                                                         GCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACT
                                                                                                                                                                                                                                                   ATTAATAATGNGATAAAATGAAATGTTAANATTTTATTTT 1153
                                                CTTTNTTTÄTTNTTNNTATTTTTTÄTNTGTTNAATATATTAAANAATTTTATGATANTTA 1113
                                                                      ACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCTTCAATTT 410
                                                                                                TNATTTATTAATAAGTTATTTACATTAATTTATTTTAGNNTNGTTTTATATAATTTGA
                    ATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTT
                                                                                                                                                                                                                                                                                                                                                     Conservative
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RESULT 11 AJ928310/c SOURCE ORGANISM VERSION KEYWORDS Locus REFERENCE FEATURES COMMENT ACCESSION DEFINITION JOURNAL TITLE AUTHORS source AJ928310 TAJ928310.1 GI:67498 EST. Theileria annulata Coulson,R.M.R., Cronin,A., de Villiers,E., Fraser,A., Fosker,N., Gardner,M., Goble,A., Griffiths-Jones,S., Harris,D.E., Katzer,F., Larke,N., Lord,A., Maser,P., McKellar,S., Mooney,P., Morton,F., Nene,V., O'Neil,S., Price,C., Quail,M.A., Rabbinowitsch,E., Rawlings,N.D., Rutter,S., Saunders,D., Seeger,K., Shah,T., Squares,R., Squares,S., Tivey,A., Walker,A.R., Woodward,J., Dobbelaere,D.A.E., Langsley,G., Rajandream,M.-A., McKeever,D., Shiels,B., Tait,A., Barrell,B. and Hall,N.

The genome of the host-cell transforming parasite Theileria annulata and a comparison with T. parva (Dontact: Pain A) The Mellcome Trust Sanger Institute
The Wellcome Trust Sanger Institute
The Wellcome Trust Sanger Institute
The Mellcome Campus, CB10 15Å, UNITED KINGDOM
Merozoite CDNA library: Frank Katzer and Brian Shiels, Division
Merozoite CDNA intram and Tmmunity, ICM, University of Glasgow, AJ928310 Theileria annulata merozoite Pain, A., Renauld, H., Berriman, M., Murphy, L., Yeats, C.A., Weir, W. Kerhornou, A., Aslett, M., Bishop, R., Bouchier, C., Cochet, M., Coulson, R. M.R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M.R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M.R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M.R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M.R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M.R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M.R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M.R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M. R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M. R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M. R., Coulson, R. M. R., Cronin, A., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M. R., Coulson, R. M., Coulson, R. M., Coulson, R. M., Coulson, R. M., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M., Coulson, R. M., Coulson, R. M., de Villiers, B., Fraser, A., Fosker, N., Coulson, R. M., Coulson, R. M., Coulson, R. M., de Villiers, B., Fraser, A., Fosker, R. M., Coulson, R. M., Co Theileria annulata tam017g02_qlk, mRNA sequence Theileria Eukaryota; Alveolata; (bases 1 to 1079) /mol_type="mRNA"
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JOURNAL COMMENT
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AUTHORS
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DU000686
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Best Local
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                                                                                                                                                                             BAC end sequencing from three Unpublished (2005)
Other_GSSs: 241792
Contact: Lukas Mueller
Tanksley Lab, Dept. of Plant B
                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
                                                           Seq primer: SP6
Class: BAC ends
                                                                                      Email: sgn-feedback@sgn.cornell.edu Plate: 47 row: O column: 2
                                                                                                                                                     Cornell University
251 Emerson Hall, I
                                                                                                                                                                                                                                                                             Mueller, L.A., Buels, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J
                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum (Solanum lycopersicum)
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           quality sequence start: 31 quality sequence stop: 283 Location/Qualifiers
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/dev stage="merozoite"
/lab_host="Bos taurus (cow)"
/clone lib="Theileria annulata
/note="country: Turkey:Ankara"
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Pred. No. 4.7;
0; Mismatches 231;
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RESULT 13
CX173493
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Best Local
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                            CX173493 698 bp mRNA linear EST:
A09_69-22_01.abl leaf inoculated with Marssonia pathogen
deltoides Populus deltoides cDNA, mRNA sequence.
                                                               Nanjing Forestry University
Longpan road 9#, Nanjing, J:
Tel: 086-025-85427412
Fax: 086-025-85427412
                                                                                                                                                                                    Leaf of poplar 
Unpublished (2004)
                                                                                                                                                                                                                                    1 (bases 1 to 698)
Huang, M., Zhang, X., Zhuge, Q.,
Zhang, B. and Wang, M.
                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
                                                                                                                                                 Contact: Minren Huang
Key Laboratory Tree Genetic
                                                                                                                                                                                                                    Identification and
                                                                                                                                                                                                                                                                                                                                             Populus deltoides
                                                                                                                                                                                                                                                                                                                                                             Populus deltoides
                                                                                                                                                                                                                                                                                                                                                                                                 CX173493.1
                                  POLYA=Yes.
                                                Bmail: mrhuang@njfu.edu.
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Location/Qualifiers
1. .698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon esculentum"
|mol type="genomic DNA"
|cultivar="Heinz 1706"
|db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="SL MboI0047002"
/lab_host="B. coli"
/lab_nost="Domato MboI BAC Library"
/note="Vector: pBeloBAC11; Site_1: MboI"
                                                                                                                                                                                                                                                                                                                                                                                                 GI:56820917
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Pred. No. 5.8;
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                                                                                                 Jiangsu,
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Saliceae; Populus.
                                                                                                                                                                                                                                                        Zhang, L., Guan, Y.,
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logen of Populus
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CE216145
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                                                                                                                                                             The Institute for Genomic Research Department of Eukaryotic Genomics, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CE216145 718 bp DNA linear GSS 25-SEP-20 tigr-gss-dog-17000373053119 Dog Library Canis familiaris genomic,
                                                                                                                                                                                                                                                                     The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                             Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CE216145.1 GI:35371814
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey
CE216145
                                                                                                     Email: ekirknes@tigr.org
                                                                                                                                                                                                                                Contact: Kirkness EF
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (dog)
                                                                                       Class: shotgun.
                                                                                                                                                                                                                                                      14512627
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                                                                                                                             301-838-0208
                                                                                                                                                301-838-0200
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/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:3696"
/clone lib="leaf inoculated with Marssonia pathogen
Populus deltoides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
/organism="Canis familiaris"
/mol_type="genomic DNA"
                                                                 Location/Qualifiers
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Pred. No. 6.4;
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                                                                                                                                                                                        TIGR,
                                                                                                                                                                                        9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 698;
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Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K Carninci, P., Shibata, K., Fukuda, S., Fukunishi, Y., Funayama, T., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Hara, A., Hayatsu, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Ocowa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV112242 215 bp mRNA li
AV112242 Mus musculus C57BL/6J 10-day embryo
clone 2610010G18, mRNA sequence.
AV112242
AV112242.1 GI:5266322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
77; Conserv
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                        Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes l
Thermostabilization and thermoactivation of the synthesis of full length cDI
trehalose and its application for the synthesis of full length cDI
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN Mouse
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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|larity 59.2%;
|Conservative
                                                                                                                                                                                                                                                          details.
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/note="Site 1: BstXI; Libraries were
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain="Standard Poodle"
              /dev_stage="10-day embryo"
/clone_lib="Mus musculus C
                                                                                                                                                                                                                             Location/Qualifiers
                                                                'sex="mixed"
                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                             organism="Mus musculus"/
                                                                                           clone="2610010G18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547
                                                                                                              xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45.2; DB Pred. No. 6.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                     C57BL/6J 10-day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepared
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Query Match Best Local Similarity 53.8%; Score 45; DB 1; Length 215; Best Local Similarity 53.8%; Pred. No. 6.8; Matches 93; Conservative 0; Mismatches 80; Indels 0; Gaps 0 296 GATTTCCAATTTATATTCCCCTATTGGGTATTTGATGGCCGTTTAAATAGTCACCAA Db 41 GAAATTTCCTTTTATATTCCTCGGAGATGTTTTTGTCCTTGAAGTCTTCACCCACACCTCA 100 Qy 356 TTGAATCTTCACTTGATCTTCGAGTTTTTGTCTCTAAAGGTCTTCAATTTATCTA 415 Db 101 ATGCACCTTTTTACTTGGAATTTTTCTGCTGCAAATTGGTCCATTGGAATTA 160 Qy 416 AAGCAAGTTTTTGTATAATTCAAAATACTTTGCTTCTCCATGGACCT 468 Qy 416 AAGCAAGTTTTTGTATAATTCAAAATACTTTGCTTTTTCTCCATGGACCT 468 Db 161 AGCCAAATGTATTTTGATGTATATACTTTGGTTTTAATAAATTTAGACT 213 Search completed: December 28, 2005, 11:15:57 Job time: 3844 secs	Sea Job	D .	₽	8	밁	Ş	3 0	J IQ
9.3%; Score 45; DB 1; Length 215; 1ty 53.8%; Pred. No. 6.8; 1servative 0; Mismatches 80; Indels 0; Gaps 1ccartinataticccctaitiggiantitigatigiacctitaaataatcacca 35 1	rch co						atche	uery !
3 3, 3 4, 3,	ompleted: December 28, 2005, 11:15:57 : 3844 secs		101 ATGCACCTTTTTTACTTGGAATTTTTTTCTGCTGCAAATGGACATTGGTCCATTGGAATTA 160	356 TIGAATCTICACTIGITCGAGTTTTGTCTTTTTGCTTCTAAAGGTCTTCAATTTATCTA 415	41 GAAATTTCCTTTATATTCCTCGGAGATGTTTTTGTCCTTGTCCCTTCACCCACACCTCA 100	296 GCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGA 355	80; Indels	Cimil ority

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
/cgn2_6/ptodata/1/ina/1_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 43.8 9.0 23672 3 US-09-949-016- 4 1.6 8.6 1358 3 US-09-270-767- 5 41.6 8.6 2267 3 US-09-270-767- 6 41.6 8.6 2267 3 US-09-270-767- 7 41.6 8.6 7218 2 US-09-270-767- 7 41.6 8.5 7218 2 US-09-270-767- 8 41 8.5 705 3 US-09-949-016- 10 40.2 8.3 113701 3 US-09-949-016- 11 39.8 8.2 640681 3 US-09-751-389- 12 39.6 8.2 786431 3 US-09-751-389- 13 39.8 8.2 786431 3 US-09-248-796A 14 39.8 8.0 564 3 US-09-949-016- 16 39 8.0 174170 3 US-09-949-016- 17 39 8.0 174170 3 US-09-949-016- 18 39 8.0 174318 3 US-09-949-016- 20 38.4 7.9 11215 3 US-09-949-014- 21 38.4 7.9 146401 3 US-09-949-014- 22 38.4 7.9 146421 3 US-09-949-016- 23 38.2 7.9 146438 3 US-09-949-016- 23 38.2 7.9 146438 3 US-09-949-016-	Result No. c 1 c 2	Score 43.8 43.8	- i a H	 	ID US-09-949-016-15296 US-09-949-016-1575	Description Sequence 1 Sequence 1
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24 38.2 7.9 146438 3 US-09-949-016-		•	٥	w	-09-949-016-12	20
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RESULT 2 US-09-49-016-12575/c ; Sequence 12575, Application US/09949016 ; Patent No. 6812339

GENERAL INFORMATION:

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36.8	36.8	36.8	36.8	36.8	37	37	37	37	37.2	37.2	37.2	37.4	37.4	37.4	37.4	37.4	37.4	37.6	37.8
7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.6	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.8	7.8
35647	20674	20674	18682	18651	50000	44353	1141	601	144922	94847	94830	1664976	1664976	199471	1856	1316	1316	237863	186959
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US-09-949-016-11896 US-09-949-016-13360	US-10-170-097-651	US-09-641-638-651	US-09-949-002-786	US-09-949-002-592	US-09-662-254B-23	US-09-949-016-15302	US-09-806-708B-22	US-09-949-016-80944	US-09-949-016-15890	US-09-949-016-16336	US-09-949-016-12414	US-09-692-570-1	US-08-916-421B-1	US-09-949-016-14083	US-09-704-725-4 ·	US-09-270-767-17763	US-09-270-767-2481	US-09-949-016-13404	US-09-949-016-13125
Sequence 11896, A Sequence 13360, A	Sequence 651, App	Sequence 651, App	Sequence 786, App	Sequence 592, App	Sequence 23, Appl	Sequence 15302, A	Sequence 22, Appl	Sequence 80944, A	Sequence 15890, A	Sequence 16336, A	Sequence 12414, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 14083, A	Sequence 4, Appli	Sequence 17763, A	Sequence 2481, Ap	Sequence 13404, A	Sequence 13125, A

ALIGNMENTS

RESULT 1

US-09-49-016-15296/c

US-09-49-016-15296/c

Sequence 15296, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

PAPPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CL001307

CURRENT APPLICATION UNUMBER: US/09/949,016

CURRENT APPLICATION DATE: 2000-04-14 밁 Ş Ś 밁 S ; ORGANISM: Human US-09-949-016-15296 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012 SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 15296 LENGTH: 23669 TYPE: DNA Query Match Best Local (Matches Match 9.0%; Local Similarity 57.8%; 9688 ATATATAGATATATA 9674 9748 АТАТТТААБАТАТТТАТАТАТАТАТСТТАРАТАТАТАТТТАРВАТАТАБАТАТАБАТАТАТАБ 9689 9808 TATATAAAGATATATATAAAGATATATAAAGATATATAAAAGATATATAAAATATAT 78; Conservative CTTTAAAGGCACATA 177 0; Score 43.8; DB 3; Length 23669; Pred. No. 0.14; 0; Mismatches 57; Indels 0; Gaps 9749

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FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12575

LENGTH: 23672

TYPE: DNA

ORGANISM: Human

US-09-949-016-12575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-49-016-14941/c
US-09-49-016-14941/c
; Sequence 14941, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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US-09-949-016-14941
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CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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Best Local :
                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14941
LENGTH: 23672
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                 Local Similarity
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78; Conserv
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                                                                                 TATATAAAGATATATAAAAGATATATAAAGATATATAAAAGATATATATAAAAATATAT 9749
                                        ATTTGAGAGGTATTTTAACACACCTTAGAACTAAAACTTAATAATAATAATATTTCTCTAT 162
  Conservative
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                                                                                                                                                               0,
                                                                                                                                                               Score 43.8; DB 3;
Pred. No. 0.14;
0; Mismatches 57;
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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                                                                                                                        ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29720
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SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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Patent No. 6639063
GENERAL INFORMATION:
                                                                                                                                                                                                 CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29720
                                                                                                                                                                                                                                                                               PATENT NO. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ESTs and Encoded Human Proteins. FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dumas Milne Edwards, APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
                                          Matches 110;
                                                        Query Match 8.6%;
Best Local Similarity 49.1%;
                                                                                                                                                                                ENGTH: 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 8.7%; Score 42; DB 3; Length 832; Local Similarity 10.3%; Pred. No. 0.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 TCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCTTCAATTTATCTAAAGCAAGTTTTGTATA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 TTCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTTCACTTGT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 TGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATTTCCAATTTATA 311
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175 ATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAAT 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRCWKKKAYYRKTTCYSSKGWTWWKRWKKAWTTWWWKKTYYWAATRYWWMMCWTKRWRAS 180
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                                            Conservative
                                          0; Mismatches
                                                               Score 41.6; DB 3; Pred. No. 0.28;
                                              114;
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RESULT 6
US-09-270-767-13702
; Sequence 13702, Application US/09270767
; Patent No. 6703491
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; Sequence 14, Application US/08232463
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                                                                                                                                                                                                                                                                                                RESULT 7
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13702
LENGTH: 2267
TYPE: DNA
                                                                                                                                                                                                          Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila melanogaster -09-270-767-13702
                                                                                                                   APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKUER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                  COUNTRY: USA
ZIP: 22313-0299
                                                                                    STREET:
                                                                                                     ADDRESSEE:
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110; Conserv
                                                                     Alexandria
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                                                                                                                                                                                                                                                                                                                                                    ATTGAAATATTGTAATGTGTTGTTTTTTTTTTTTCGTTCTTTTAA 2229
                                                                                                                                                                                                                                                                                                                                                                                     ATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAA 398
                                                                                                                                                                                                                                                                                                                                                                                                                          TAGATTTGTAAGTCGCCTTCAACTTATTGTTGTTGTTTATTCGCTGAGCTTAATGACAT 2185
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                                                                                    1800 Diagonal Road,
                                                                                                                                                                                                             DORNER, F.
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                                                                                                      Foley & Lardner
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                                                                                      Suite
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US-10-030-808-1

Sequence 1, Application US/10030808 Patent No. 6887677 GENERAL INFORMATION:

APPLICANT: Taylor, Ronald K.
APPLICANT: LaPointe, Christian F.
APPLICANT: Trustees of Dartmouth

APPLICANT: Trustees of Dartmouth College TITLE OF INVENTION: COMPOUNDS AND METHODS

OF IDENTIFYING COMPOUNDS WHICH

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Best Local Similarity 4.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEFAX: 899140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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COMPUTER: IE
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                                                                                                                                                                                                                                                                                                                                                  173 ACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAA 232
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YGTACCAAATTCTTCTATCTCTTTAACTACTT 1465
                              CTAAAGCAAGTTTTGTATAATTCAAAATACTT 444
                                                                                                     CGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCTTCAATTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.6%; Score 41.6; DB 2; ilarity 4.3%; Pred. No. 0.4; Conservative 208; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-09-949-016-15328
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                                   ; OTHER INFORMATION: n = US-09-949-016-15328
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 15328 LENGTH: 111235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15328, Application US/09949016 Patent No. 6812339
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Query Match
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CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 60/143,355
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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TYPE: DNA
ORGANISM: Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001307
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                       ORGANISM: Human
                                                                                                                                             TYPE: DNA
                                                                                    NAME/KEY: misc_feature
                                                                                                          FEATURE:
                                                                     LOCATION:
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                                                                      (111235)
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Pred. No.
Score 40.6;
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Length 111235;
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US-09-949-016-13214
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US-09-949-016-13214/c
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                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                          GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: SAKAKI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows SEQ ID NO 13214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13214,
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Matches 67; Conserv
                                                                                                                                                                                                                                                                      Sequence 1, Application US/09790988 Patent No. 6632935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                 NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
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LENGTH: 640681
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0; Mismatches
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Length 981;

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RESULT 12
US-09-751-389-3
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                                                                                                                                                                      RESULT 13
US-09-248-796A-1989/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature; LOCATION: (1)...(786431); OTHER INFORMATION: n = A,T,C or US-09-751-389-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09751389
Patent No. 6630334
GENERAL INFORMATION:
Sequence 1989, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
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Best Local Similarity
Matches 78; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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US-09-248-796A-486/c
US-09-248-796A-486/c
; Sequence 486, Application US/09248796A
; Patent No. 6747137
; Patent No. 6747137
; GENERAL IMPORMATION:
    APPLICANT: Keith Weinstock et al
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT APPLICATION NUMBER: US 60/074,725
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
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SEQ ID NO 486
LENGTH: 564
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SEQ ID NO 1989
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PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
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                                                                                                                                                                      Local Similarity
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                                                                                                231 AAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTAT 290
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                               CTGTGGCATTTCCAATTTATATTCCCC 317
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     CTTGGGCATATTTATAGCAACTTTACC 445
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Pred. No. 1.1;
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Pred. No. 1
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Indels

Gaps

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RESULT 15
US-09-949-016-14810/c
Sequence 14810, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FRANCESCO FOR WINDOWS Version 4.0
SEQ ID NO 14810
TYPE: DNA
OPGANITAM: Human
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; FEATURE;
; NAME/KEY: misc_feature
; LOCATION: (1)...(174170)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14810
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Search completed: December 28, 2005, 11:18:48
Job time : 163 secs
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                                                                                                                               159 CTATCTTTAAAGGCA 173
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Minimum DB
Maximum DB
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                                                                       seq length: 0
seq length: 2000000000
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
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9.7 3254 6

9.7 3259 6

9.6 1223197

9.6 1223197

9.5 523197

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9.5 6092 7

9.2 37211 6

9.2 517 8

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Copyright (c) 1993 - 2005 Compugen Ltd.
5 7 US-10-600-230-1
4 5 US-10-600-230-81
4 6 US-10-027-632-114994
4 6 US-10-027-632-179264
9 7 6 US-10-027-632-179264
9 7 US-10-027-632-179264
9 6 US-10-311-455-91
2 7 US-10-33-793-28
1 6 US-10-33-345A-1843
7 8 US-10-363-345A-1843
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9 US-10-27-632-208958
9 US-10-027-632-208958
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9 US-10-221-714A-429
1 US-09-925-065A-77681
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Sequence 1, Appli
Sequence 81, Appl
Sequence 114994,
Sequence 1179264,
Sequence 179264,
Sequence 179264,
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 1843, Ap
Sequence 1843, Ap
Sequence 1844, Ap
Sequence 1844, Ap
Sequence 1843, Ap
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Sequence 100, App
Sequence 100, App
Sequence 1100, App
Sequence 1107, App
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Sequence 123, App Sequence 557010,		Sequence 386, App	Sequence 135303,	Sequence 135302,	Sequence 135303,	Sequence 135302,	Sequence 554823,	Sequence 238494,	Sequence 621748,	Sequence 1, Appli	Sequence 135, App	Sequence 97, Appl	Sequence 1, Appli	Sequence 653223,	Sequence 3, Appli	Sequence 3, Appli	Sequence 681, App	Sequence 17809, A	Sequence 673, App	Sequence 89, Appl

US-10-600-230-1

Sequence 1, Application US/10600230 Publication No. US20040092020A1 GENERAL INFORMATION:

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| CAMBRAL INFORMATION: | CAMBRAL INFORMATION: | APPLICANT: Wilkinson, Jack | APPLICANT: Wilkinson, Sean | TITLE OF INVENTION: GENETIC CONSTRUCTS HAVING HETEROLOGOUS | TITLE OF INVENTION: GENETIC CONSTRUCTS HAVING HETEROLOGOUS | TITLE OF INVENTION: J. POLYADENYLATION SIGNAL SEQUENCE MOTIFS THAT FUNCTION IN TITLE OF INVENTION: PLANTS | FILE REFERENCE: 0325.210 | CURRENT APPLICATION NUMBER: US/10/600,230 | CURRENT FILING DATE: 2003-06-20 | PRIOR APPLICATION NUMBER: 60/330,529 | PRIOR FILING DATE: 2002-06-20 | NUMBER OF SEQ ID NOS: 81 | SOFTWARE: Feature | Sec ID NO 1 | SEQ ID NO 1 | LENGTH: 485 | TYPE: DNA ORGANISM: Saccharomyces cerevisiae | US-10-600-230-1
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241 AACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCACTATTTATCTGTGGCATT
                                                                                  181 CGTGGCTAAGGCAATTACAGCTGATATACTGTAAAAACTCATGTCGCCCACTAAATTCTTCT
                                                                                                                                           121 CÁCACCTTÁGAACTÁÁAACTTÁATAATAATATTTCTCTÁTCTTTAAAGGCACATATTA
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RESULT 2
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Publication No. US20040092020A1
GENERAL INFORMATION:
APPLICANT: Wilkinson, Jack
APPLICANT: McBride, Kevin
APPLICANT: Bertain, Sean
TITLE OF INVENTION: GENETIC CONSTRUCTS HAVING HETEROLOGOUS
TITLE OF INVENTION: JACANTS
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 81
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Best Local (
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CURRENT FILING DATE: 2003-66-20
PRIOR APPLICATION NUMBER: 60/390,529
PRIOR FILING DATE: 2002-06-20
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Similarity 99.6%;
76; Conservative
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      ACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCTTCAATTTATCTAAAGCAAGTTT
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Pred. No. 3.8e-101;
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                                       425
Sequence 114994, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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US-10-027-632-114994/c
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RESULT 3
US-10-027-632-114994/c
Sequence 114994, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR PELLOR DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 114994
LENGTH: 3254
                                                                                                                                                                                                                                                                                                                                                Query Match 9.7%;
Best Local Similarity 55.1%;
Matches 92; Conservative
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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                                                       TTATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTTTCTCC 455
                                                                                                                                                                                                                                  ATCTTTAATTTAGATAATGTATTTTTACTTCTAGAATTTTAATTTGGCTCTTTTTAAAG
                                                                                                                                                                                                                                                                                         ATCTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTGGCCGTTTAAATAG
TTATTTAAAGATCTTGTATGTTAATTCTATATGTGTAGTTTTGCTTC
                                                                                                                 TCTTCATTTCTATGCTGAAATTCTCCATCTTTTTCTCTAAATTCTTTAAAATGTTATGAT
                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 1.1;
0; Mismatches 7
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1326
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24

APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23

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US-10-027-632-179264/c ; Sequence 179264, Application US/10027632 ; Publication No. US20020198371A1
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US-10-027-632-114994
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SEQ ID NO 179264
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Best Local Similarity
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                 Query Match
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 2000-02-24
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(1223197)
OTHER INFORMATION: n = A,
                                                                                                                                                         ORGANISM: Human
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Local Similarity
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APPLICATION NUMBER: US 60/146,002
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9.6%;
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Pred. No. 1.1;
0; Mismatches 7
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Score 46.4;
Pred. No. 1
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13;
                   DB 5;
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78 ATATATGGTTGTGTGAACTTATTTATTTGAGAGGTATTTTAACACACCTTAGAACTAAA 137

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US-10-027-632-179264/c
                                                                                US-10-027-632-179264
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
PRIOR PPLICATION NUMBER: US 60/185,218
PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILLING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 179264, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                SOFTWARE: FASTSEQ
SEQ ID NO 179264
LENGTH: 1223197
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                    Best Local Similarity
                                     Query Match
                                                                                              TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1223197)
OTHER INFORMATION: n = A,T,C o:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTTAATAAATATTTCTCTATCTTTTAAAGGCACATATTACGTGGCTAAGGCAATTA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATATATGGTTGTGTAACTTATTTTATTTGAGAGGTATTTTAACACACCTTAGAACTAAA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTGGGTATTTGATGTGGCCGTTTAAATAGTCACCGATTGAATCTTCACTTGTTCGAGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMIMIMIMIMIMIMIATIATCGTCGTCGCATTTGAGAATTGGAYKYTTCTCTATCGAAA 1195627
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  Conservative
                                                                                                                                                                                                                                                             Windows
                    9.6%;
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98
Score 46.4; DI
Pred. No. 13;
86; Mismatches
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                                       DB 6;
    182;
                                         Length 1223197;
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US-10-311-455-691
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-691
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Publication No. US20030143606A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 691
LENGTH: 5739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
PILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR PILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, CI APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                 Local Similarity
211
                                                                 151
                                                                                                  789
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                                                                                                                                                                                               31 TTGCGTAGACAGTATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTG
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GTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACT 270
                                                                                                                               TMTMTMTMTMTMTAATTÄTCGTCGTCGCATTTGAGÄÄTTGGAYKYTTCTCTÄTCGAÄÄ 1195627
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                                                               ATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACT
                                Conservative
                                                                                                                                                                                                                                               9.5%;
45.9%;
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                                                                                                                                                                                                                                                 Score 46.2; DI
Pred. No. 2.1;
                                                                                                                                                                                                                                 Mismatches 228;
                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                               Length 5739;
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CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: PCT/EP01/02945
DE 10013047.00
DE 10019058.8
DE 10019058.8
DE 10019058.8
DE 10032529.7
JE 10043826.1
PRIOR FILING DATE: 2001-03-15
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NUMBER OF SEQ 1
SEQ ID NO 36
LENGTH: 6092
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Publication No. US20040029123A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BERLIN, Kurt TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle FILE REFERENCE: 5013.1004
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: chemically treated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-04-06 2000-04-07
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               TGTTGTATTTTATAATTTATAATAGTAATAAAATATGA---
                                                                               AAATTGATATAATATAATATTGTATATTTTTTTTATTAAATTTTTGTTTTAAAAATTTTTAAA
                                                                                                              GTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTA 241
                                                                                                                                                  ACACCTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIEPENBROCK, Christian
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                 Score 46.2;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                               DB 7;
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                                                                                                                                                                                                                                                                                                                                                                   (Homo sapiens)
                                                                                                                                                                                                                                                                                                                 Length 6092;
                  -TAATTATTTGTGTGAAAT
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Sequence 309, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Ass
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: CTIPE01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
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US-10-433-793-28
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US-10-311-455-309
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Best Local S
Matches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/433,793
CURRENT FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 28
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
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TITLE OF INVENTION: Diagnose von mit Angiogenese
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                  14199 T
                                                                                                                                                                                                                                                                                                                                                                                                             14139 AATTTTTTGTTAATTTTCGGTAGTTTAAGAAATTGAATGGAGTAGGTAATGATATTAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATG
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; Pred. No. 7.8;
0; Mismatches
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LENGTH: 7201
TYPE: DNA
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Matches
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SEQ ID NO 1843
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: chemically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 517
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Local Similarity 53.4%;
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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        344
                                                                                                                                                             183
                                                                                                                                                                                            164
                                                                  284 TATTTATCTGTGGCATTTCCAATTTATATTCCCCTATTGGGTATTTGATGTGGCCGTTTA 343
                                                                                                 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTTACTGTGATACTTACAA
                                                                                                                                                                                                                                                                                                                    94;
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      AATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCTAAAGGTCT 403
                                                                                                                              CGCCACTAAATTCTTCTAACACGCGTTCTGTCTCTTTCCAAGGGACTCCGAATATGCCAC
                                                                                                                                                             TTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGT
                                                                                                                                                                                                                          TAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAA 189
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CURRENT APPLICATION NUMBER: U$/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 1844
LENGTH: 517
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 1844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1844, Application US/10363345A Publication No. US20040234960A1 GENERAL INFORMATION:
Sequence 1843, Application US/10363483A
Publication No. US20050064401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 174; Conservative
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Best Local Similarity
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APPLICANT: Christian Pie
APPLICANT: Kurt Berlin
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INVENTION: Diagnosis of illnesses
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Pred. No. 2.3;
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RESULT 14
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CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 1843
LENGTH: 517
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 174;
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FILE REFERENCE: 82011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: chemically treated
OTHER INFORMATION: CpG-island No: 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.2%;
Local Similarity 44.6%;
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                                                     CGTTTTTTTTTTACGTTATTTTTCGTTTAT
                                                                            TCAATTTATCTAAAGCAAGTTTTGTATAAT 433
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                                                                                                      Conservative
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Pred. No. 2
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Sequence 1844, Application US/10363483A
Publication No. US20050064401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or
TITLE OF INVENTION: illnesses
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
                                                                       ; FEATURE:
OTHER INFORMATION: Chemically
OTHER INFORMATION: CpG-island
US-10-363-483A-1844
                                                                                                                                             SEQ ID NO 1844
LENGTH: 517
TYPE: DNA
ORGANISM: Artificial Sequence
Query Match 9.2%;
Best Local Similarity 44.6%;
Matches 174; Conservative
 Score 44.4; DB Pred. No. 2.3; 0; Mismatches
 0;
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No: 1844
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Sequence 53227, Application US/09925065A

PUBLICATION NO. US20050228172A9

GENERAL INFORMATION: US20050228172A9

GENERAL INFORMATION: Identification and Mapping of Single

FILLE OF INVENTION: Identification and Mapping of Single

FILLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

FILLE REFERENCE: 108827.135

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-03-09

NUMBER: US 60/289,846

PRIOR FILING DATE: 2001-05-09

NUMBER: US 60/289,846
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53227
LENGTH: 1803
TYPE: DNA
ORGANISM: Homo sapiens
S-09-925-065A-53227
                                                                                                                                                                                                               Query Match 9.0%; Score 43.8; DB 4; Length 1803; Best Local Similarity 50.7%; Pred. No. 4.9; Matches 105; Conservative 0; Mismatches 102; Indels 0
168 AAGGCACATATTACGTGGCTAAGGCAATTACAGCTGATATACTGTAAAACTCATGTCGCC 227
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                                                                                             129 AGAAATATGTTATTCTTCACCAGCAAGATGTTGGGTGGTAGTGTGTAATACATCTTTTAT
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Search completed: December 28, 2005, 11:32:43 Job time: 825 secs

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381 Sequence 46381, A RESULT 2
Sequence 93, Appl US-10-240-708-62
438 Sequence 36438, A ; Sequence 62, Application US/10240708
438 Sequence 40, Appl ; Publication No. US20050282157A1
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Copyright (c) 1993 - 2005 Compugen Ltd. ic search, using sw model cember 28, 2005, 09:24:36; Search time 293 Seconds (without alignments) 867.750 Million cell updates/sec 10-600-230-1 gcggcgggaaggaagtcctccaaatgatgaggtacc 485 ENTITY NUC pop 10-0, Gapext 1.0 72979 segs, 262114271 residues ts satisfying chosen parameters: 8345958 igth: 0 igth: 0 igth: 2000000000 iinimum Match 08 iaximum Match 1008 isting first 45 summaries
model 24:36; Search time 293 Se (without alignments) 867.750 Million cellcctccaaatgatgagg 0 1 residues parameters: 8345958
model 24:36 ; Search time 293 Se (without alignments) 867.750 Million cell cctccaaatgatgagg 0 1 residues 1 residues 8345958
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- 2005 / model
- 2005
GenCore version 5.1.6

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US-10-750-185-3073 US-10-750-185-3340	US-10-750-185-44880 US-10-995-561-13286	US-10-750-185-38146	US-10-750-185-24697	US-10-995-561-13421	US-10-276-233A-13	US-10-750-185-24875	US-11-117-187-211	US-10-750-185-58341	US-10-995-561-42981	US-11-121-086-77	US-10-995-561-13278	US-10-750-185-58628	US-10-750-185-50592	US-10-516-768-15	US-10-240-708-20	US-11-121-086-50	US-10-750-185-52828	US-10-995-561-13199	US-10-793-626-3453
Sequence 3073, Ap Sequence 3340, Ap	Sequence 44880, A Sequence 13286, A	Sequence 38146, A	Sequence 24697, A	Sequence 13421, A	Sequence 13, Appl	Sequence 24875, A	Sequence 211, App	Sequence 58341, A	Sequence 42981, A	Sequence 77, Appl	Sequence 13278, A	Sequence 58628, A	Sequence 50592, A	Sequence 15, Appl	Sequence 20, Appl	Sequence 50, Appl	Sequence 52828, A	Sequence 13199, A	Sequence 3453, Ap

ALIGNMENTS

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RESULT 1

US-11-121-086-79

Sequence 79, Application US/11121086

Publication No. US20050266459A1

GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
FILE REFERENCE: 09138.6000-00000

CURRENT FILLING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

PRIOR APPLICATION NUMBER: 60/567,570

PRIOR FILING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: Patentin version 3.3

SEQ ID NO 79

LENGTH: 177175

TYPE: DNA

ORGANISM: Homo sapiens
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Best Local Similarity
Matches 97; Conserv
76790 TTTTAATTT 76798
                                                                                             76730 ATTCTAGATCTCATGATÄATCTGTÄÄCACTTCTTTTAACTCAATÄGAAGTÄATTCCTCTG 76789
                                                                                                                                                                                                                                                                                             76610 TCCTGCTACATATÁCATTTTTCAAAAACAGCTTGACTGTTATGCTTAAAATGTGATATAT 76669
                                                                                                                                                                                             76670 TATTTCATGTAATTTATATTCAATAAAATTAATCTAAAAAGATTAATAAAAAGGATTTAG 76729
                                               204 ATATACTGT 212
                                                                                                                                             144 TAAATAAATATTTCTCTATCTTTAAAGGCACATATTACGTGGCTAAGGCAATTACAGCTG 203
                                                                                                                                                                                                                                   84 GGTTGTGTGTAACTTATTTTATTTTGAGAGGTATTTTTAACACACCCTTAGAACTAAAACTTAA 143
                                                                                                                                                                                                                                                                                                                           24 TCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACTTACAAGTTGATATAT 83
                                                                                                                                                                                                                                                                                                                                                                                     8.6%; Score 41.8; Dilarity 51.3%; Pred. No. 1.2; Conservative 0; Mismatches
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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILTE OF INVENTION: by Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION UNMER: US/10/240,708
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-09-01
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Sequence 90, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
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Best Local Similarity
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               APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 98
PRIOR APPLICATION NUMBER: 60/567,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5418
                                                                                                                                                                                                                                                                                                                                                                                   5658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 ACACACCTTAGAACTAAAACTTAATAAATAATATTTCTCTATCTTTAAAGGCACATATT
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                                                                                                                                                                                                                                                                                                                                       AAGTTTTGTATAATTCAAAATACTTTGCTTTT 451
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Pred. No. 0.52;
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APPLICANT: BATES, Stephen
APPLICANT: PANTIN, Dennis
TITLE OF INVENTIN, COMPOSITIONS FOR INFERRING BOY
FILE REFERENCE: MMILION-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR TILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
PRIOR FILING DATE: 2002-12-31
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                                                                                                     US-11-117-187-188/c
                                                                                                                       RESULT 5
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LENGTH: 1303
TYPE: DNA
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NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.0%;
Best Local Similarity 52.5%;
Matches 85; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50224, Application US/10750185 Publication No. US20050260603A1
                                               Sequence 188, Application US/11117187 Publication No. US20050266560A1 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 148220
TYPE: DNA
APPLICANT: PREUSS, DAPHNE
APPLICANT: COPENHAVER, GREGORY
TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIN version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACTTACAAGTT
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                                                                                                                                                                                                                                             351 ACCGATTGAATCTTCACTTGTTCGAGTTTTTGTCTTTTGCTTCTCTAAAGGTCTTCAATTT 410
                                                                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATATATGGTTGTGTGAACTTATTTGAGAGGTATTTTAACACACCTTAGAACTAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ААСТТААТАААТААТАТТТСТСТАТСТТАААGGCACATAT 178
                                                                                                                                                                          ATCTAAAGCAAGTTTTGTATAATTCAAAATACTTTGCTTTTCTCCATGACTTGAACCT 468
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                                                                                                                                                                                                                                                                                                                   Conservative
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57.6%;
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                                                                                                                                                                                                                                                                                                                                    Score 38; I
Pred. No. 2.
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; Sequence 84, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
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; AAME/KEY: modified base
; LOCATION: (2720)...(72695)
; OTHER INFORMATION: N = A, C G, or T/U
US-11-117-187-188
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CURRENT APPLICATION NUMBER: US/11/117,187
CURRENT FILING DATE: 2005-04-28
PRIOR APPLICATION NUMBER: US/09/531,120
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 1999-03-18
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 212
                                                                                                                                                                                                                                                                           SEQ ID NO 84
LENGTH: 118996
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Best Local Similarity
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Best Local Similarity
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LENGTH: 95223
                                                                                                                                                                                                                       -11-121-086-84
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APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OP INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
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                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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   9770
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GCCGTTTCAAATCTTTTCTGAAATAAACAAGATACACATAAAGGTGTAAAATGATGTCAT 9829
                                    TCTTTCTATATTCATTCTCATTTCTAAAGGTATGTGTCTGGGTTATTTTTACCCTTGTAA
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                                                                                                                                             7.8%; Score 38; DB 7; Length 118996;
45.8%; Pred. No. 8.9;
ative 0; Mismatches 155; Indels 0
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Pred. No.
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RESULT 8
US-11-121-086-105
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US-10-750-185-55780
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                                                                     Sequence 105, Application US/11121086
Publication No. US20050266459A1
GENERRAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR TILING DATE: 2004-05-04
PRIOR TILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: MMI1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 55780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
                SOFTWARE: PatentIn version 3.3 SEQ ID NO 105
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                                                         NUMBER OF SEQ ID NOS: 107
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
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LENGTH: 171486
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mes 77; Conserv
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KERR, Richard
ROSENFELD, David
HOLM, Tom
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-105
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US-10-750-185-64497

; Sequence 64497, Application US/10750185

; Publication No. US20050260603A1
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; ORGANISM: Bovine
US-10-750-185-64497
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US-11-121-086-39
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APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
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Best Local Similarity
Sequence 39, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 64497
LENGTH: 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILLING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
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TITLE OF INVENTION: COMPOSITIONS FOR INFERRING
FILE REFERENCE: MMI1100-2
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Local Similarity 58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 TCTTTAAAGGCACATATTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 TATGAAAATATTTTTACTGTGATACTTACAAGTTGATATATGGTTGTGTGTA-ACTTATT 101
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HOLM, Tom
BATES, Stephen
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Pred. No. 14;
0; Mismatches 56; Indels
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; NUMBER OF SEQ ID NOS: 107
; SOPTWARE: PATENTIN VERSION 3
; SEQ ID NO 39
; LENGTH: 207835
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-39
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US-11-121-086-40
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.3 SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: POULSEN, XIM S.
APPLICANT: NIELSEN, KIRSTEN V.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patrant
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 207835
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                                                                                                                                                                                                 138 АСТТААТАААТААТАТТТСТСТАТСТТТАААСССАСАТАТТАССТСССТААСССААТТА 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 ATATATGGTTGTGTGAACTTATTTATTTGAGAGGTATTTTAACACACCTTAGAACTAAA
                                                                                                                  198 CAGCTGATATACTGTAAAACTCATGTCGCCACTAAATTCTTCTAACACGCGTTCTGTCTC
                                                                                                                                                                                                                                                                               78 ATATATGGTTGTGTGTAACTTATTTATTTGAGAGGTATTTTAACACACCTTAGAACTAAA 137
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                                                                            ATATTTATATTGTGTTAACCTCATTTACCAAGACATTTCAAATTTACATCTTTGTGTCTG
                                    TTTCCAAGGGACTCCGAATATGCCACTATTTAT 290
TTAAAGACAGATTTAGAAATACACTAATTTTAT 200100
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                                                                                                                                                                                                                                                                                                                                                 Score 37; DB Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 207835;
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US-10-995-561-73227/c

RESULT 12

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; ORGANISM: Bovine
US-10-750-185-30231
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US-10-750-185-30231
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APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, GENERIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS

TITLE OF INVENTION: DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO 73227
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOPTWARE: PatentIN version 3.1
SEQ ID NO 30231
LENGTH: 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30231, Application US/10750185
Publication No. US20050260603A1
GENERAL INFORMATION:
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Best Local 9
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APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MMI1100-2
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MMI GENOMICS,
APPLICANT: DENISE, Sue F
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, De
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TYPE: DNA
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120
                                                                                                                        283
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                                       AAATAGTCACCGATTGAATCTTCACTTGTTCGAGTTTTGTCTTTTGCTTCTCAAAGGTC 402
                                                                                                                        CTATTTATCTGTGGCATTTCCAATTTATATTCCCCCTATTGGGTATTTGATGTGGCCGTTT 342
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ACTCATTGCTCTATTTAAATTACACTTGGTCTTTTTGACAATTTTGTTTCATAACAATTA 179
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                                                                              CTCGCTCTTAGTGGCATTCCCTAGTCATCTTAACATTTTTCATATCTAAATTTAATAGAA 119
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KERR, Richard
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50.9%;
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Pred. No. 4.8;
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Pred. No. 2.9;
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APPLICANT: KERR, Richard

APPLICANT: ROSENFELD, David

APPLICANT: HOLM, Tom

APPLICANT: HOLM, Tom

APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MMI1100-2

CURRENT APPLICATION NUMBER: US/10/750,185

CURRENT FILING DATE: 2003-12-31

PRIOR APPLICATION NUMBER: US 60/437,482

PRIOR FILING DATE: 2002-12-31

NUMBER OF SEQ ID NOS: 64922

SOFTMARE: PatentIN version 3.1
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US-10-995-561-13443/c
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                                                                                                                                                                                                                                                    Sequence 13443, Application US/10995561
publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 39457
LENGTH: 1588
                                                                                                                     CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                      FILE REFERENCE: CL001559
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ORGANISM: Bovine
                                                             ORGANISM: Homo sapiens
                                                                                   LENGTH: 49979
TYPE: DNA
NAME/KEY: misc_feature
LOCATION: (1)...(49979)
                                           FEATURE:
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Local Similarity 50.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 CAAGTTGATATATGGTTGTGTGTAACTTATTTATTTGAGAGGTATTTTAACACACCTTAG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 GGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACTTA 70
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Pred. No. 6.8;
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                                                                                                                                                                                                                                                                                 DRUG RESPONSE,
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,	Wed Dec 28 15:29:20 2005 us-10-600-230-1.
; OTHE	; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-995-561-13443
Query Best I Matche	Query Match 7.5%; Score 36.2; DB 6; Length 49979; Best Local Similarity 50.3%; Pred. No. 19; Matches 86; Conservative 1; Mismatches 84; Indels 0; Gaps 0;
유 성	9 AAGGAGGAAAGTGACTCCTTCGTTGCGTAGACAGTATGAAAATATTTTTACTGTGATACT 68
	TACAAGTTGATATATGGTTGTGTGTGAACTTATTTATTTGAGAGGTATTTTAACACACCCTT
ş	
β Q	43936 TTAAATGGATACAAAATTGCTGTGTAAAATAMGTGTTTTCAAAATACATTTCTATAGGTA 43877
Q B Q	TTAAATGGATACAAAATTGCTGTGTAAAATAMGTGTTTTCAAAATACATTTCTATAGGTA 43877 AGAACTAAAACTTAATAAATAATATTTCTCTATATCTTTAAAGGCACATATT 179
0 Db 0 Db 0 Db 0 Db	TTAAATGGATACAAAATTGCTGTGTAAAATAMGTGTTTTCAAAATACATTTCTATAGGTA AGAACTAAAACTTAATAAATAATATTTCTCTATCTCTTATAAGGCACATATT 179
Oy Db Qy Db Search c	THAATIGATACAAAATIGCTIGTBAAAHAMGIGTTTTCAAAAAIACTATAGGTA 43877 AGAACTAAAACTTAATAAATAATTTCTCTATCTTTTAAAGGCACATATT 179
Oy Oy Db Db Search o	MGIGITITICAAAAIACAITICTAIAGGIA 43877 TAICTITAAAGGCACAFAIT 179 : TAITAICAAAASTAICTAIT 43826
Oy Oy Oy Db Search c	MGIGITITCAAAATACATTICTATAGGTA 43877 TATCTITAAAGGCACAFATT 179 : TATTATCAAAASTATCTATT 43826
Db Db Qy Db Search c	MGIGITITCAAAATACATITCTATAGGTA 43877 TATCTITAAAGGCACAFATT 179 : TATTATCAAAASTATCTATT 43826
Oy Oy Oy Db Search o	MGIGITITCAAAATACATTICTATAGGTA 43877 TATCTTTAAAGGCACAFATT 179
Qy Qy Db Search c Job time	MGIGITITICAAAATACGTATATT 179

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

The Popo Blonk (Usolo)